

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6675	277	1678	GNWPTERMAFLDNPTIIIAHIRQSHVTSDDTGCMEMVLIHDHDVD LEKIHPSSMPGDSGSEI0GSNGETOGYVYQAQSVDITSWDFGIR RRSNTAQRLEI.RKERQNIQKCKNQI0KERNNSKQSAECKSLFE KKSLKEKPPISGKOSILSVRLEQCPQLNPNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMVVMTMASARVQDQLIGLICWQ YTSEGREGPKLNNDNVSAYCLHIAEDDGEVTDFTFPLDSNEPIHKF GFSTLALVEKYESPGLTSKESLFRVIRNAAHGFSLIQVDMNTKVTM KEILLKAVKRKGSKVGSRADGVFEEDSQIDIAVTQDMLSSH HYKSFKVSMIHLRFTTDVQL/GCALFPGLVRKRAAPVDCLRPS ADTWRQEIGCCGAACAALRS*DSHKC*EG1SGDKVEIDPVTNQ KASTKFWIKQKPFISIDSLLCAC\DAEE
6676	277	1676	GNWPTERMAFLDNPTIIIAHIRQSHVTSDDTGCMEMVLIHDHDVD LEKIHPSSMPGDSGSEI0GSNGETOGYVYQAQSVDITSWDFGIR RRSNTAQRLEI.RKERQNIQKCKNQI0KERNNSKQSAECKSLFE KKSLKEKPPISGKOSILSVRLEQCPQLNPNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMVVMTMASARVQDQLIGLICWQ YTSEGREGPKLNNDNVSAYCLHIAEDDGEVTDFTFPLDSNEPIHKF GFSTLALVEKYESPGLTSKESLFRVIRNAAHGFSLIQVDMNTKVTM KEILLKAVKRKGSKVGSRADGVFEEDSQIDIAVTQDMLSSH HYKSFKVSMIHLRFTTDVQL/GCALFPGLVRKRAAPVDCLRPS ADTWRQEIGCCGAACAALRS*DSHKC*EG1SGDKVEIDPVTNQ KASTKFWIKQKPFISIDSLLCAC\DAEE
6677	277	1678	GNWPTERMAFLDNPTIIIAHIRQSHVTSDDTGCMEMVLIHDHDVD LEKIHPSSMPGDSGSEI0GSNGETOGYVYQAQSVDITSWDFGIR RRSNTAQRLEI.RKERQNIQKCKNQI0KERNNSKQSAECKSLFE KKSLKEKPPISGKOSILSVRLEQCPQLNPNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMVVMTMASARVQDQLIGLICWQ YTSEGREGPKLNNDNVSAYCLHIAEDDGEVTDFTFPLDSNEPIHKF GFSTLALVEKYESPGLTSKESLFRVIRNAAHGFSLIQVDMNTKVTM KEILLKAVKRKGSKVGSRADGVFEEDSQIDIAVTQDMLSSH HYKSFKVSMIHLRFTTDVQL/GCALFPGLVRKRAAPVDCLRPS ADTWRQEIGCCGAACAALRS*DSHKC*EG1SGDKVEIDPVTNQ KASTKFWIKQKPFISIDSLLCAC\DAEE
6678	221	865	GPSNQSSGSSLELVTGCGSS*INDTCTILRVLSNNGFRQ*LR PPFCSDQPLMSQGLCWHLDCCCPVWVPIPGQWRKGQRMRN*QS LLGSDQESVGLEDLVCVFVNLLHVLLGLFP*PHELFLPVVDLG FLFLPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLOTHDEGSRN HHPLFLVGRMELAVKHELTQVSGSLASLGFGVQHTSHGGP
6679	2	786	LEFARGAMPFLGODWRSPGQNWVKTVDGWRKFLDEKSGSFVSDL SSYCKEVYNKENFLFNSNLYD/SCSQEEKEGAE*ONONS\DFH QEKWYVHKGSTKERHGCTLGEAFNRQDFSTAILEDSSRRFNYVV RLLLELIAKSQTLSLGIAQKNFMNILEKVLVVLKDQONITLIR ELLQFTLTSCLTVKRVGKSVLWVGNIWMMWVYRMETIHLWQQQNI NIQITRVGQAOOPPGGSGSLHRDTQTRDFEPTVTEESGLF
6680	1498	2951	PLCTLPPLMPSAL\WGAERWEK0PLA/PGPGTWTOPVGSISEE P\RKNEPDTHCPGEARPEV*HLPKPHSPGSEGAEI0TSA*ALP /NQVSPPPQPM*GAEENGDQRGGKEEAGEEILHRSSSGLTAAPGF? EVHRRNLOTFPGLPSRGGGP/GGACTGQSWAPGEQPP/SPLLPAS MQRSGQAGLPGWEAGLVESPTHHIFALRPGSGTNATGEAFPSTTCS SGP*PAPPGPTGLRPGGSSSSGGG*PGLPVGV\GALGAAQD PQSOGRGPTQGTVGTEMILSGLGSAKACPAARPAPV*LPSPDPAS TIPKKGTRGFGECPGVLOERNRWWVGRAQGFTSADAAGTAPPGV *LPAPLSSOPPGATEPQVRAKGMAFPSPGTSGRVLVANGRHPGPQV AQGCPPGAGCWCSQPRGSQRCRPTYTHSPLGHGRAPCPRCRW WQDPSSPRTGCLPGIPARQAYASAPRTSRSPGIRTRGAAVYGF FOGGGGG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6681	1169	511	INYYIYNNQQQRAFHELK\EKLMASAPALGLPDLTKLFTLHVSE KMTVGVLTOTVGPWSRPGAYLSQLDGVSKGWPPCPRALAATAL LAQEADELTLRQNLRNKSPhA\VVTLINTKGHH*LINARLTRYQ TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDVYS SRPNLRLDHP*TSVWDWLYVDSGSGFANPCKVTLKETSPAPVTPR S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLEPEWLSDRKKRALQKDVD VRRRIELIQLDFEMPTVCTTIKVKSDGQYILATGTYKPRVRCYDT YOLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG FYYKTRIPKFGDRFSYHYPSCDLYFVGASSEVYRLNLEOGRYLN PLQTDAEENNVCIDINSVHGLPATGTIEGRVECWDPRTRNRVGLL D\AP*TVSQOIQR*TSLPTISALKFN\GALTMAVGTIGQVLLY DLRSDKPLLVKDHQYGLPIKSVHFQDSDLILSADSRIVKMWNK NSGKIFTSLPEHDLNDVLYPNSGMILLTANETPKMGIIYIPV GPAPRWCSFLDNLTLEELENPESNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLEPEWLSDRKKRALQKDVD VRRRIELIQLDFEMPTVCTTIKVKSDGQYILATGTYKPRVRCYDT YOLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG FYYKTRIPKFGDRFSYHYPSCDLYFVGASSEVYRLNLEOGRYLN PLQTDAEENNVCIDINSVHGLPATGTIEGRVECWDPRTRNRVGLL D\AP*TVSQOIQR*TSLPTISALKFN\GALTMAVGTIGQVLLY DLRSDKPLLVKDHQYGLPIKSVHFQDSDLILSADSRIVKMWNK NSGKIFTSLPEHDLNDVLYPNSGMILLTANETPKMGIIYIPV GPAPRWCSFLDNLTLEELENPESNE
6684	113	527	GLRGGTSGRAGREPEFAAGVLCVVAFCQSPCPGGRRGREAPA PP\SGRRHRA\*RPA\*WLCGGPGGDSGGREEGGS\GELQRAMESKMG ELPLDINIQEPRWDQSTFLGRARHFFTVDPRNLLSGAOLEAS RNJVQNYR
6685	256	1473	KLLGDNFEGFCNKFELSDSENGSNS\QSP\FDRLFDPDPQKV LQVIDMKNAVIGNNKQKANLIVLGAVPRLYLLQQETSSTELKT ECAVVLGSLAMGTENNVSLLDCHIIPALLQCLLSPDLKFIAC LRCLRTIFTSPVTPPEELLYTDATVIPHLMALLSRSRYTQEYICQ IFSHCCKGPDHQTIILVNGAVQNIJAHLITLTSYKVRMQLAKCFS VLFENPQVSMTLVNVLVDGEELLQPIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKLTPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELORIASITDHJAMLAQYFVPSVSAITDIK RLDHDLKHAELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL TASROGVITST
6686	310	927	DSVTFDLDAVDFTPKEWTLLDPTQRNLYRDVMLENYKLNATVGY QLFKPSLISWLEQEEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTTSGIOMGSHNGGEVSDVKOCCDVSSHEHSLKTHVRTON SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCOKNRCTRKKAF\*LQTLGKSFH\*SIHT
6687	181	915	EAMLEAPYKKEDEDEOQKEVKDDYPSNTTSSTSNSGNETSGSST IGETSNSRDKDRYRRNRSRSPGRQCRHRSRSWDRRHGSESRR SRDHRRDRVHYRSPLATGEPVDNLSPPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAVEFCEIQSV PLAIGLTGQRLLGVPVIIQASQAENRLLAAMANNLQKGNGGPMR LYVGSLLHFNITEDMRQGIFEPFGKV
6688	1025	1	AEVPNYPRVFHCKCPDSCWRFKFQPIQLQPYILLFSSEKPPISF SEPGLPR\SATARMATAAAPPNNSSIDLPDSGMGFIS\PGDSDL LPSDGTTGFFSLAGDSSTRLSSLAIFI\FSLSSVSVGSSAGTT STSVGSVVAFTSSSSSTNRDVAGLDFSTVITSVGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTAATAASSMPSGTSSFSTC TMSELEELFSLPSPAPLILSKLFTSSCSIAICQDSCFSDTGRLS VCQLWLAQSDTGLKLSDCQEVVTVGDGGGLTCPPELSLGRM\*MSLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SSAVIPGYSSSSDSRLNTVPTVLLCPFQTKSST
6689	640	1299	SSSASVATSATISDTAFSGSLKLKHGLLSALDSSSRTS*STSS AEDSTFRICSPSPVSDTSSDSSGSKDNVLLIFSKVSI*SCFSLSS FFSDSISFCSSSSFCRK*FVSSKVSQNALLSSRLSGPGGSSK ORNSLTLAROLAMSL*ATKF*RNA:CNPNCLSSKKSL*LSLNQRF GGSASRKPGNISFNSQKCSALSYCCNFV1KPREVSVSSENYPAF
6690	3	442	GTRGKMAATLGPLGSWQWRRCILSARDGSRMLLLLLLGSGQGP QOOGAGOTFEYKLKREHLSLSPYQGVGTGSSSLWNLMGNAMVMTQ YIRLTPDMQSKQGALWNRVPCFLRDWEELQVHFKIHGQGKKNL\H GDGLAIWYTKDRMQP
6691	287	1401	LKTETSEKARRYKDRPQLSQLNAVFQEQKKMIAQAESITLEDVAV DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALK LEQGEOLWTIEDGIHSGACSDIWKVDHVLERLOSESLVNRRKPC HEHDAFENIVHCSKSQFLLGQNHDIFDLRLGKSLKSNLTLVQNSK GYEIKNSVEFTGNGDSLHJANHERLHTAIKFPASQKLISTKSQF 1SPKHKOTRKLEKHVCECGKA:FIKKSWLTDHQVMHTGEKPHR CSLCEKA:FSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRSLNI HOKTHTEGKPYICSECGKGFIQKGNLIVHQRINTGEKPYICNEC /GKGFIQKTCILAHQRFLINTER
6692	176	939	WIKEGELSLWERFCAN11KAGPMPKHIASFIMDGNNRKYAKKCQVE RQEGHSQGFNKLAETRLRWCCLNLG1LEVTVYAFSIENFKRSKSEV DGLMDLARQKFSRIMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL 1AQAVQATKKNYNKCFLNVCFAYTSRHEISNAVREMAVGVEQGLL DPDSDISESLLDKCLVYTNRSPHPD1LIRTSGEVRLSDFLLWQTSH SCLVFCFVLLWPEYTFWNLFEAILOFQMNHSVLQK
6693	176	939	WIKEGELSLWERFCAN11KAGPMPKHIASFIMDGNNRKYAKKCQVE RQEGHSQGFNKLAETRLRWCCLNLG1LEVTVYAFSIENFKRSKSEV DGLMDLARQKFSRIMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL 1AQAVQATKKNYNKCFLNVCFAYTSRHEISNAVREMAVGVEQGLL DPDSDISESLLDKCLVYTNRSPHPD1LIRTSGEVRLSDFLLWQTSH SCLVFCFVLLWPEYTFWNLFEAILOFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSPQPLSSVSTETASSVRQAAESRQHELPVRE VHSLGQ1LPQDGLTAEAGPPEAQDPNGSPG1SLPAHIGFAAA LAVGPGSCHTEP\1FDEWPSLFLGDAYAARDKSKL1OLGITHVV NAAAGKFQVDTGAKFYGRMSLEYGYIEADDNPFFDLISVYFLP
6695	292	813	SLLLHLAPPGAYTPSPQPLSSVSTETASSVRQAAESRQHELPVRE VHSLGQ1LPQDGLTAEAGPPEAQDPNGSPG1SLPAHIGFAAA LAVGPGSCHTEP\1FDEWPSLFLGDAYAARDKSKL1OLGITHVV NAAAGKFQVDTGAKFYGRMSLEYGYIEADDNPFFDLISVYFLP
6696	3	782	PRVRGRVGERWAFLSVPAAMSSEMPILLAWSYFRRKFOLCAD LCTQMLEKSPYDOAAILKARALTEMVYIDEIDVDOEGIAEMML DENAIQAVPRPGTSLKLPGTNQGGPSQAVRP1TOAGRPIGFL RPSTQSPRGTMEOQAI1PRTAYTARP1TSSSGRFVRLGTASML TSPDGPF1NLSRLNLTKYSQPKLAKALIEY1FHHENDVKTALD LAALSTEHSQYKDWNNWK/DQIEKCYYRVMGRYREAEKOIKSS SL\SGGEFSSQNTVNLNSLEDLKPF1LLNDMEHLWSSLNSNCK
6697	3	782	PPLFLRRLNSRLRPGSRKVMAVVPASLSQDVGFSFAYLT1KDR 1PQILTKV1DTLHRHKSEFFEKHGEEGVAAEKK1SLLSKLRNE LQTDKPF1PLVKEKFVDTDIWNQYLEYQQSLLNEDGKSRWFYSP WLLV\ECYMYRRIHEAT1IQSPP1IDYFDVFKESKEONFYGSQES 11ALCTHLQQLIRTIEDL\ENQLDEFFKLLQ1SLWGEISVDSL SL\SGGEFSSQNTVNLNSLEDLKPF1LLNDMEHLWSSLNSNCK
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6699	325	492	EGELP/PARRVLPRAWTASAQPRGRRPGVGVGVVVTSCKHPRCV L1GKRGKGSVGAGGSFOLPGGHLEFGETWECAORETWEAALHLK NVHFASVNSFIEKENYHYVT1LMKGEVDVTHDSEPKNVEPEKN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6700	1096	1392	ESKRRIYNHAFFFQESKWSGGJLQ TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMMDTNECIQ FPFVCPDRKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT LLLGLCNLLGK
6701	2	1485	AAAGPTRTRVRRAAAFEQGPSPSPGLGPTSDKAAPRTPKRRRLW RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRIGI IEVDYFGLQFTGSKGESLWLNLRNRIISQMDGLAPYRLKLRLVKF FVEPHLILQEQTTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA QTKEFGDYNONTAKYNYEELCAKELSSATLNSIVAKHKELEGTQS ASAEYQVLQJIVSAMENYGIIEWHSVRDSEQKLLICVGPEGISIC KDFDFSPNRIAYPVVQMATQSGKVNLYLTVKESGNNSIVLLFKMI STRAASGLYRAITETWAFYRCDTVTSAVMMQYSRDLKGHLASLF LNENINLGKYYVFDIKRTSKVEVYDHARRALYNAVGVVDLVSRNQ SPSHSPLKSSSESSMNCCSCEGLSCQTRVLQEKLRLKKEAMLCM VCCEEEINSTFCPCGHTVCCESCAAOLOVGEAAHFCLOPHLSL LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLEPMEDVFLFYRTFCMSMGLGSSCHLSPK RAEALLCSRKATVVRLDVAVRMAEEQEFTQLCKLPAQPSHPCV NNTYRSAQHSQALLRCLLALRDSGILFDVVLVVEGRHIEAHRIL LAASCDYFKGMPAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS ELELSLSNVQETLVAACOLQIPEIIFCCDFLMSWDEENILDV YRLAELFDLDSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET VRFPLMEEAVLQLRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ SPQTELRSDFQCVVGGIHSHTPS\MSSATRPKYLNPLLGEWKH FTASLA PRMSNQGIAV LNNFVYLIGDNNVQGFRAESRCWRYDP RHNRWFQIQLQQEHADLSVCVVGRIYIYAVAGRDIYHNDLNNAVER YDPATNSWAYAPLKREVYAHAGATLEGKMYIITCGRKGRT
6703	45	1244	GVGPRAAAMPLELECPGRWVGQHPCFIIAEIGONHQGDLDA KRMIRMAKECGADCAKFOKSELEFKFNRKALERPYTSKHSWGKT YGEHHRHLFSDHQYRELQRYAEVEGIGFTTASGMDMAMVEFLHE LNPFFKVGGDTNNFPYLEKTAK/TRCWHSVLRDVCGVQLNDE TSSWDVLGRVRSTSKEVKLMLVLDYSGRPVIVSSGMQSMDTMQ VQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP IGYSGHETGIAISVAVALGAKVLERHITLDKTWKSDHSASLE PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGSVVAKV KIPEGTILTMMDMLTVKGEPKYPPDEDIFNLVGKKVLVTVEEDD TIMEE
6704	82	1007	TMNTRNRRVNSGLGASPASRPTRDPODPSCRGEGELSPVEDOREG LEAAPKGPSRESVVIAGORRRTSAYTTLIAPNINRRNBIQRIABQE LANLEWKWEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK YKQKLKREESVRIKEAEEAELQKMKAIQREKSNKLEEKKRLQE NLRREAFREHQYKTAEFL/RQTEHRIAROKCLSCKCLWPTILN MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKROQQEQE RAKIHOTEHRRVNNNAFLDRLOGKSQPGGLEQSGGCWNMSGNSW GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGF1GPLRGPHPRAGGTGTSFT SYKRKGIGIMSTIAAFYGGKSLILITVATGFLGKELMEKLFRTSPD LKVIYILVTPKAGQTQHHRVFQILDSKLFEKVIEVRPNVHEKIR AIYADLNQNDFAISKEDMQEILLSCTNIIIFHCAATVRPDDTLRA VQLNVATRQLLIMASMPKLEAFIHISTAYSNCNLKHIDEVYI PCPVEPKKIIDSLEWLDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	PTHSSSSHSQEMLGKLNMLRNDGHFCDTITRVQDKIFRAHKVVL AACSDFFRTKLVGQADEDENKNVLDLHHVTVTGFIPILLEAYATAT LSINTENIIDVLAASYSQMFVASTCSEFMKSSILWNTPNSQP EK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6707	223:	1343	YWSGIGYELQHFWRKFHFEEKKGPSTCQBERLYESRSRWP CIS* GMVVGWTA VNGSW* CGOLRCV CVC TSHSSDSTRSSORASKCHS FFILSQ* KT* SSWENWVFAKYSR IYSYGHCSKGRGD* DFK* NV SQAR* SRPCGLCNP CGH CGLD1NLRGGSSPWTDKHSCVHNLLC NRRVFSLLC ECPGHCYQGAVCREACAAASPGLD SAE PHLCEH TD* LPK* GPGYI QHFCDSN1LCL YNISF NLYSF* GVAR YA C* RCHWY FEWLLY NHCGDILVACL* RQOL* SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAQSPQGGM ALQVELVFT GEIIRVPHPRPC KLA LGS DGV RVT MESA TARD RVG VQDFVLL ENFTSEA AFENLRRKFR ENLYT YIGPV LVS VNP YRDI QIYSR OHMERYRGVSPYEEPPHLLVADTVY RALR TERRDQAVMISVES GAGKTDATKRLQ LQYAE TCA PAP QRGVA VRDR LQSNP VLEAFGN AKTLRNDN SRS FGK YM DVQ FDF KGA? VGGHILS YLLE KSRV VH Q NHGERNFHIFYOLLEG EEE TLR RLGLER NPQ SLYL VNG QOC AK VSSINDKSDW KVVR KALT VDFT DEVED LLSIAAS VHL GN IH FAANEESNAQVTTENQ LKYLTRLLS VEG STI REAL THRK IIA KG ELLSPLN LQ EAA YAD ALA KAV SRT FTL VLG KIN RSL ASK DV ESPSWRSTTVLGLL D IYGF E VQHNS FE QFC INYC NEK LQQLF I ELTLKSE OEE YEA E C I AWE P VQY F NNI I C D L V E 2 K F G II \ S I LDE \ ECL R PGE
6709	3	894	PPHEHLPFGSGERGPFSFLV SRRGLGP GKG KKE KKG RGA EK TAAKMEKKVSKRSRKEE DLE ALIAH F QT LDA KRT Q T VEL PC PP PSPLRN ASL SVH PPEK D L I L F G G E Y F N G Q K T F L Y N E L Y V N I R K DTWTKV D I P S P P P R C A H Q A V V V P Q O G G Q L W V F G G E F A S P N G E Q F Y H Y K D L W V L H L A T K T W E Q V K S T G G P S G R E G H R M V A W K R O L I L F C G F H E S T R D Y I Y N D V A F N L D T F T W S K L S P S G T G P T F R S G C Q \ I P S L P R A S S V Y V G G Y S K Q R V K K D V D K G T R H S D M F
6710	158	980	RHKMTN YR VESS SGR A R K M R L A L M G P A F I A I G Y I D P G N F A T N I QAGASFGYQLLSAKVNWL MAMLIQ I L S A K L G I A T G K N L A E Q I RDHYP R P V V W F V W Q A E I J A M A T D L A E F I G A A I G F K L I L G V S L L Q G A V L T G I A T F L I L M L Q R R G D K P L E K V I G G L L L F V A A Y I V E L I F S Q P N L A O L G K G M V I P S L P T S E A V F L A A G V L \ G A T I M P H V I / Y I W H S S L T Q H L H G G S R Q C R Y S A T K W D V A I M T I A G P V N L A I M T A A A S E L N F Y G H T G V A
6711	3	347	VTECKT M TCK M S Q L E R N I \ T M I N T L H H Y S V K L G H P D T L I H G E P K E L V R T D L H N I L M K E N K N D Q A I \ H I M E D L D T N A H M Q I I F K E L I M L M A M L T W S Y H D N M H D A Y G P G Q O H R P G
6712	118	578	PHGQKRTRYFQV RAP QO P Q A O L A M A L C L K Q V F A K D K T F R P R K R F E P G T Q R F E L Y K K A O Q S L K S G L D L R S V R L P P G E N I D W I A V H V V D F F N R I N L I Y G T M A E R C S \ T S C P V M A G G P R Y E R W Q D E R Q Y R R P A K L S A P R Y M A L L M D W I E S L J
6713	2485	3	Q A R G S D E I G E F I Q A E D D A R A R K L G P G R P L P T F P T S E C T S D V E P D T R E M V R A Q N K K K K S G G F Q S M G L S Y P V F K G I M K G Y K V P T P I O R K T I P V I L D G K D V V A M A R T G S G K T A C F L L P M F E R L K T H S A Q T G A R A L I L S P T R E L A L Q T L K F T K E L G K F T G L K T A L I L G G D R M E D Q F A A L H E N D I I I A T F G R I V H V A V E M S L K L Q S V E Y V V F D E A D R L F E M G F A E Q L Q E I I A R I \ P G G H Q T V L F S A T L P K L L V E P A R A G L T E P V L I R L D V D T K L N E Q L K T S F L V R E D T K A A V L L H L L H N V V R P D Q T V V F V A T K H A E Y L T E L L T T Q R V S C A H I Y S A L D P T A R K I N L A K F T L G K C S T L I V T D L A A R G L D I P L L D N V I N Y S \ P A K G K L F L H R V G R V A R A G R S G T A Y S L V A P D E I P Y L L D L H L F L G R S L T L A R P L K E P S G V A G V D G M I L G R V P Q S V V D E E D S G L O S T L E A S L E L R G L A R V A D N A Q Q Q Y V R S R P A P S P E S I K R A K E M D L V G L C L H P L F S S R F E E E E L Q R L R L V D S I K N Y R S R A T I F E I N A S S R D L C S Q V M R A K R Q K D R K A I A R F Q Q G Q Q G R Q E Q O E G P V G P A P S R P A L Q E K O P E K E E E E E P A G E S V E D I F S E V V G R K R Q R S G P N R G A K R R R E E A R Q R D Q E F Y I P Y R P K D F D S E R G

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LSISGEGGAFEQQAGAVLDDLMGDEAQNLTRGRQQQLWDRKKR FVGOSQEDKKK1KTESGRYISSSSYKRDLYQKWKQKQKID* <sup>S</sup> L GRRGILTRRRPRTEEVGEARPLAQAGCIPGPHAPRHPQAE LELKTKQOILKORRAOAAKSLQRWPQAAALCPQ
6714	169	1416	NNCQELLPPPPAPMAHIPSAGAAPPAPGQYCVCKVELSVS GQNLLDRDVTSKSDPFCVLFTEENNGRWEYDRTEAANNLNPAF SKKFVLDYHFEVQKLKFALFDQDKSMRLLDEHDFLQFSCSLG TIVSSKKITRPLLNNDKPAGKGLITIAAOELSNDRVTILSLAG RRLDKKDLFGKSDPFLFVYKPGDDGKWMVLVHRTVEVYKTLDPVW KPTFVPLVSLCDGDMEKPIQVMCYDNDGHDFIGEFQTSVSO MCEARDSPVLEFECINPKKQRKKNYKNSGIIILRSCKINRDYS FLDYILGCCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL SAIWAVGQI1QDYDSKDMPALGFGAOLPPDWKVSHFAINFNP TNPFCGVDGIAQAYSACLP
6715	32	493	GPAGAESGLIHCLPATVQALAGAAHSPHGGOPPRRGPLJGSGMP GKPKHGVPNGRMVLAVSDGELSSTTPQGQGEGRGSSLSIHS PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEPS AENVTFWKACERFQOJPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKMSARA AAKSTAMEETAIWEQ HTVTLHRSLLCSK
6717	115	896	LFAMSGENLNLDYQTSYISDDOSQSYDYGGSGGPYSKQYAG YDYSQQRFPVPPDMQMPQQPYTGQIYQPTQAYTPASPQPFYGN FDEPPPLLEELGINFHDWQKTLTVLHPLKVADGSI NETDLAG PMVFCLAFGATLALLAGKQFQGYVYGI SAIGCLGMFCLLNLMMSMT GVSFGCVA SVLGCLLPMILLSSFAVIFSLQGMVGI ILTAGIIG WCSFSASKIFISALAMEQGQQLLVAYPCALLYGVF ALISVF
6718	290	599	KQSSSTVPGTILPSLKW HNSGLCKFFETGGKMTTFKEGLTFKDVA VIFTEEELGLLDPVORNL YQDVMLENFRNLLS VGHHPFKHDVFL LEKEKKLDIMKTATO
6719	1	691	PTREEQDREDGCKH KMMEMNPISGNLNC DPIAMSQCSSDHG CET DLDSDDDKIE KPNFM KDSASQDN CLSLRK ISRK VCSS DSDSSL QVVK KSS KART GLLR ITR RC ATA AANK KIK LMSD VED VS LEN VHT RS KNG RIKK PLH LACT TAK KLS DCE GSV HCE VP SE QY ACE GK PP DP DSEG STK VLS OAL NGD SD ED MLN SEH K HR HT NI HK ID AP SK RK SS V T SS V TSS
6720	3	822	HEVAEEAGGT VY PORG T MPGT KRF FOH VIET PEPG KWE LTG YEAA VP ITE KS NPL T Q D L D K A D A E I V R I L L G Q C D A E I F Q E E Q A L S T Y Q R E S I L T T M V Q V A G K V Q E V L K E P D G G L V V L S G G T S G R M A F L M S V S F N Q L M K G L Q K P L Y T L I A G C D R S V V A S R E G T E D S A L H G I E E L K V A A G K K R V I V I G I S V G L S A P F V A Q M D C M N T A V F L P V L V G F N P V S M A R H F P P P R I L R S L T V F P S L R A P H Y Q I T S L L F S M S V T L I S E
6721	3	822	HEVAEEAGGT VY PORG T MPGT KRF FOH VIET PEPG KWE LTG YEAA VP ITE KS NPL T Q D L D K A D A E I V R I L L G Q C D A E I F Q E E Q A L S T Y Q R E S I L T T M V Q V A G K V Q E V L K E P D G G L V V L S G G T S G R M A F L M S V S F N Q L M K G L Q K P L Y T L I A G C D R S V V A S R E G T E D S A L H G I E E L K V A A G K K R V I V I G I S V G L S A P F V A Q M D C M N T A V F L P V L V G F N P V S M A R H F P P P R I L R S L T V F P S L R A P H Y Q I T S L L F S M S V T L I S E
6722	1	390	RSWSKR T W Q A L P M A V L F L L F L C G T P Q A D N M Q A I Y V A L G E A V E L P C P S P T L H G D E H L S W F C P A A G S F T T L V A Q V Q V G R P A P D P G K P G R E S R I R L L G N Y S L W L E G S K E E D A G R Y W C A V L G Q H H N Y Q N W
6723	173	659	VCQYCTARMADFG I S A G Q F V A V W D K S S P V E A L K G L V D K L Q A L T S G L S A E I A R I L R P G G C F L K E P V E T A V D N N S K V K T A S K L C S A L T L S G L

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			VEVKELQREPLTPEEVOSVREHLGHESDNL
6724	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFPDIILSGLVPGSTTLHSAEIL AEIARILRPGGLFLKEPVEAVDNNSKVKTASKLCSALTLSGL VEVKELQREPLTPEEVOSVREHLGHESDNL
6725	356	722	RRRTPPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD ASWELVDPPTPDOLALFVQFNDQFFWGCL2AVEVKWSVRMTLCAG ICSYEGGGMCSIRSLPPLLKLRLPRKD1VEVFFV
6726	98	714	HLQKMERKINRREKEKEYEGKHNSSLEDTDQGKNCCKSTLMTLNVG GYLYITOKCTLTQVDPDTLEGIVNGKILCPFDADGHYFIDRGL LFRHVLNFRLRNGEPLLPEGFRENQLLAOEAEFFQLKGLAEEVKS RWEKEQLTPRETTFLEITDNHDRSQQGLRIFCNAPDFISKIKSRI VLVSKSRLDGFPPEEFSISSLN1QFKYFIK
6727	1	831	FRGMGDERPHYYGKHTGPKYDPTFKGPIYNRGCTDIICCVFLL LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP YLFYFNIVKACASPLVLEFQCPPTPQICVCEKCPDRYLTLYNARSS RDPEYYKQPCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF PAIAYKGVLVGMNETTYEDGHGSRKNIITDLVEGAKKANGVLEA RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILRLRFLAGIMG RGMIIMGILVLVG
6728	486	935	FCSSWLSLADSSLWSKMKFLVGLTGGIASGKSSVIQVFQOLGCA VIDVDVMAHVVQPGYPAHRIIVEVFGTEVLLENGDIRKVLGD LIFNQPDRLQOLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRTD
6729	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRLLLGTVTGFLAOSV LAGVKKFDVPCGGRDCSGGCOCYPEKGGRCQPGPVPGQGYNGPP GLOQFPGLQGRKGDGERGAPGVTPKGVDVGARGVSGFPGADGI PGHPGQCGPRGRPGYDCNGTQGDSGPQGPGSEGFTGPPGPG PKGQKGEPYALPKEERDRYRGEPEGLVGFQGPPGRPGHVQGM GPVGAPCRGPPGPPGPKCQGNRGLGFYGVKGKEKDVGQPGPN GIPSDTLHPIIAAPTGVTFHPDQYKGEKGSEGEPEGIRGISLKGEE GIM
6730	784	1015	NMVDYYEVGLORYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDYDKYGETGLNEF
6731	1	446	GIRKRLHGAVVPRVEVGPWETRESEGVLHERPTSLKNNDDEGS LDIYAGLDSAVSDSASKSCVPSRNCNDLYEEILTECTAKEATY NDLQEVEYKGQLQMKELKKFKEIQTQNFSLINEQSLKKNISA LIKTRATEINRKEDEEI
6732	102	1205	GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGRPTPPRSHRRHROEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLLAPQNGGSSDAPAYFTPPSRQGRREVRFSDEPPEVYDFE PLVAKERSPVGKTRLLEFRSDSAKEEVRESAYYLRSRQRROPR POETEEMKTERTRLQQQHSEQPLPQSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKTKVRSIQEAPAVSEDLVIRLRRPLRYPR YEATSVQOKVNFSSEGEETEEDDQDSSHSSVTTVKARSRDSDSEG DKTTRSSQYIESFW
6733	613	1311	RSCRQVGMRSRNQGGEASDGH1SCPKPSTIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVHMLKTEKTPKEVLEAHYGSQPEKVLR VLHRDIALAOEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRTVYELENEKHKC:TDYMNKSDDFTNLLEQERERLKK LLEQEKEYQARKE
6734	189	551	SAAMFPVSGCFQELQEKNSLELVSFEEVAVHFTWEWQDLD AQRTLYRDVMLETYSSLVSLGHCTKPEMIFKLEQAEPWIEE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSILVELCEVHLV
6735	280	558	KSRRAGVTKMSNPNFLKQVFNKDKTFRI KRKFEPGTQRFELHKKA QASLNAGLDLRLAVOLPPEGEDLNDWVA VHVDFFNRVNLIYGTI XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLKKLSSVLPPLITDYVYFEN SSSNPYLIRRIEELNKTAGNVEAKVVCFYRRRDISNTLIMLAD IYAKEIEESETTVEADLTDKQKQLKRELFLSRQYESL.PATH IRGKCSVALLNETESVLSYLDKEDTFYSLVYDPSLKTLLADKG EIRVGPRYQADIPLEMLEGTFPCVFAV
6737	150	1209	PVIMPLHFSPGDIVRSPCCVSSSPKLERNAHSRLESYRPDTDSL REDTGCNLQHISDRENIDDLNMEPNPSEHPRASTI FLSKSQTDV REKRKSLSFINHPPGQIARKYIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN PEQKQIYRFVRLTSAAQLTAECAIVTIVYLERLILTYAEIDICP ANWKRIVLGAAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE RQFLELLQFVNINVPSSVYAKYFFDLRSLAEANLSPLEPLSRE RAHKLEAJSRJ.CEDKYKDLRSLRSARKRSLADNLTLFRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEM PGSGLAVFLAVLVLL WGAPWTHGRRSNVRVITDENWRELLEGIWMEFYAPWCACQNL QPEWESPAEWEGLDELEVNIAKVDVTEQPGLSGRFIITALPTIYHC KDGEFRRYQGPRTKDFINFISDKEWKSIEPVSSWF
6739	3	631	SWPDMAEVEEVALKEHMLLRQEYVVKLCKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQQYSDLKIKVGRDRHESAHKF VLAARSDWSLANSSTKELDLSDANPEVTTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEVEEVALKEHMLLRQEYVVKLCKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQQYSDLKIKVGRDRHESAHKF VLAARSDWSLANSSTKELDLSDANPEVTTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAHTGMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAVQPVSILGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNQLCQRIFOVNAPINCVCVLPNQAEELIVGDQSGAIHW DLKTDHNEQLIPEPEPEVSITSAHDPAASYMAAVNSTLVPFSCLL PLAIGILQEGEFESELARRGLLFLACQGNCYVWNLTGGIGDEVTO LIPKTKIP
6742	141	960	PLTLPFSSRARAHTGMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAVQPVSILGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNQLCQRIFOVNAPINCVCVLPNQAEELIVGDQSGAIHW DLKTDHNEQLIPEPEPEVSITSAHDPAASYMAAVNSTLVPFSCLL PLAIGILQEGEFESELARRGLLFLACQGNCYVWNLTGGIGDEVTO LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPKMPKRISISKQLASVK ALRKCSDELKAIATTALIPRNNSSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDLFDLDFMILLSLITVMSDL LQNR
6744	95	1343	RTPARNRCAGCEVLSRFSSPKKASSFALCSAGGGPAVRALRRD ROKVSTVGYGMDEVEQDQHEARLKEFLFDSDITGTGSLQOEELT DLCHMLSLEEAVPVLQQTLLQDNLLGRVHFQFKEALILLILSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRSLPEFQESVEEFPE VTVIEPLDEEARPSHIAAGDCSEHWKTOSEEEYEAEQOLRFWNP DDLNASQSGSSPPQDWEEKLOEVCEDELGITRDGHILNRKKLVSI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CEQYGLONVDGEMLEEVFENLDPDGTMSEDFFYGLFKNGKSLT PSASTPYRQLKRHLMSMQSFDESGRTTTSAMTSTIGFRVFSCL DDGMGHASVERILDTWQEEGIENSQEILKALDPGLDGNIINTEL TLALENELLVTKNSIHQACI
6745	1	588	TFRDOGWAQRRRLLGCAWSWEAAIAAGPGLPSSTARQONNP AAGTCTAAVWAWRGCTAMGSVLSTDGCKSAPASATARALERRDP ELPVTSFDCAVCLEVLHQPVTRCGHVFCSRSCIATSLKNNKWTC PYCRAILPSEGVPATDVAKRMKSEYKNCACEDTLVCLSEMRAHI RTCOKYIDKYGPLOEDETA
6746	110	492	GATGAMAESAPAKHRRKRRSTPLTSSTLPSQATEKSSYFQCTEI SLWTVVAAIQAVEKMKMSEQARLQSLEGRGTGAEKKLADCEKMA VEFGNQLEKGWAVLGLTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDDLAQRKLYRDVMLENFRNLLSVGH QPFHRDTFHLREEKFWNMMDIATOREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEEELGLLDDLAQRKLYRDVMLENFRNLL LSVGNQPFHQDTFFFLGKEKFWKMKTSQREGNSGGKIQIEMET VPEAGPHEEWSCQGIWEQIASDLTRSQNSIRNSSQFPKEGDVPC QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGDGVCPRARGSPQSQFPSCAGGEGLQOSGEALDGAM SAGGCPAAAGGGPGGASCVGAPGGVSMFRWLEVLEKEFDKAF VVDVLLIGEIDPDDADITYEGRQKMTS'LSSCPAOLCHKAOSVSO INHKLEAQIQLVDLKSELTETQAEKVULKEVHDQLLQHLSIQLQL HAKTGQSAADSGTIKAKLSPSVEELERELKAN
6750	3	428	SCESRPGAKNWWSGALPRDTTGLGEQPSGDVAOSNRATMGT TAPGPIHLLLCDQKLMFLCNMDNKLVLWLEIQQEAEERMFTR EFSKEPELMPKTPSKNRRKKRRIYVQDENRDPPIRRRLSRRKS RSSQLSSRR
6751	152	1417	PTKATEMAGASVKAVRVRPFNSREMSRDSKCTIIQMSGSTTTIV NPKOPKETPKSFSPDYWSHTSPEDINYASQKQVYRDIQEEML QHAFEGYNYVCIFAYGQTGAGKSYTMMGKOEKDQGIIQPLCEDL FSRINDTTNDNMSYSVEVSYMEIYCEVRDLLNPKNKGNLRVRE HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS SRSHAVFNIIFTQKRHDATETNITTEKVKSJSLVDLACSERADST GAKGTRLKEGANINKSLLTLLGKVISALAEAMDGPNNKKKKTD FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSLR YADRAKOIRCNAVINEDPNNNKLIRELKDEVTRLRDLLYAQGLGD ITDMTNALVGMSPSSSLASLSSRNV
6752	24	1834	RNCVPPILGCYRSRVKPHSDIKMQYSHHCEHLLERLNKOREAGFL CDCTJYVIGEOFQKAHRNVLASFSYFQGAIYRSTSENVFLDOSQ VKADGFQKLLEFIYTGTNLDSWNVKEIHOADYLKVEEVVTKC KIKMEDFAFIANPSSTEIISITGNIELNOQTCLLTRDYNNEK SEVSTDLLQANPKQGALAKSSQTKKKKAFNSPKTGQNKTQY PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVKRKGKQSOPNCALKEHSMNSIAVKSPYAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRRIHKGVKPYV CHLCGKIAFTQCNQLKTHVTRHTGEKEYKCELCDKGFAOKCQLVF HSRMHIGEEKFYKDCVNCNQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRHRTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSAED HTLSEQDSIQKSPSLSETMDVKPSDMTLPALPLGTEDHHMLLPV TDTQSPSTDTLLRSTVNGYSEPQLTFLQQLY
6753	2	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPPVMPGGEKA PFGIKLRRNTYSLRFNCDDQQAEEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHPGSLPQERKQAPSTRRDSAEPPSSRSVP AHPGPPASSQTPAPEHDKAANKMPLAOKPALAPKPTSQTTPAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLSKLSPYLVLELLSRAGRPDPPEPSEPSKEDQESSDRRPPSPP GPEERKGQKRDEEEEATERKPASPPPLPATCOEKPSQTPEAGRKE KPMQLQSRHSLDGSKLTKVETAQPLWITLALQOKQKGREQQATR EERKQAREAKOAEKLSKENVSVSVPQGSSSVSRAGSLHKSTALP EEKRPETAVSRERREQLKKANTLPTSVTVFISYSSPAAPLVKE VSKRFSSPDDAPVSSPEPAWLAALKAKAWDCPLIIK
6754	2	413	YVRRRRRLGGPEVNTMSSLHKSRIADFDQDVLKPESTALEKLRE LSFSGSIPCEGGRLCLCWKILLNLYPLERASFTSILAKQRELYAQ FLREMIIPQGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD NEVLL
6755	296	1343	PGLQLOVALEADWFLDMFGGRRGSPSRQQLERSALPSLQTLVGGG CGNGTGLRNRRNGSAIGLPVPPITALTTPGPVPHCQIPDLPVQGS LLFEFLFFIYLLVALFIQYINIYKTVWWPYNHPASCTSLSNPHL IDYHLAAPITVMLARRLVWALISEATKAGAAAMIHYMVLISARL VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYFFGVVYFLCCFHQ DSRAHLLTDYNYVVQHEAVESASTVGGLAKSKDFLSLLLESL KEQFNNATPIFTSHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS LFSAYYVAFPLCPFKVKGVLTFMCFLDLCVRYINNUVFLV
6756	180	754	TERALGSLPLSIPVWSGSLRTLKYQQQPLRFKVLLCQTRVQCHD LRSLQPOPPGLKOSFCLRVLGLQOTGATTGPGRLDLTCKELIILTE REAQKRKRKEKESGMALTOQPLTFRDVAIEFSQEEWKSLSDPVQ KALYWDVMLENYRNLVFLGKDNEALEVKICFRVFLYFLCCLSWE PFHYLTSTEALLTHK
6757	2	459	NSRVEAPEAHKSRESOGSDAMRKHLSSWWIATVCMILFLSHLSAVQ TRGIKHRIKWNRKALPSTAQITEAQAENRPCAFIKQGRKLDID FGAEGNRYEANYWQFPDCIHYNGCSEANVTKEAFVTCINATQ AQNQGEFQKPDNKHLHQQVJW
6758	1	1008	ASGPPELPGRRFRDRAPWLPARLLRGVLAVWVSLSLALGPGSFCRR RVPSLAQGLHSEAAPSPDDVRWSRVPDRCPEDRAWFPPPPPS LPPSFRRNAMMSPALTGNNSQPOHOAAAAACQQQCGGGGATK PAVSGKOGNVLPWGNEKTMNLLNPMILTNILESSPYFKVOLYELK TYHEVVDIEYFKVTHVPEWKGSRKTAGQTGMCGGVGVGTGGI VSTAFCLLYKLFTLKLTRKQVMGLITHTDSFYIRALGFMYIRYT OPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE WFSTLFPRIPVVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLSSPVPORKTOSGCFDLDSS LLHLKSSFSRSPRCLNIEDDPDIHEKPFLSSAPPITSLSLLG NFEESVNLNRFDPLGIVDGFTEAVGAGFCPTHLTPVEVSFY SVSDDNAPSPYMGVITLESGLKRGYVPPSGTIQVUCVL
6760	239	606	VISSKKKGLSAEEKKTRMMEIFSETKDVFQLKDELEKIAPIKEKGIT AMSVKEVLQSLVDDGMVDCERIGTSNYWAFPSKALHARKHKE VLESQLEGSQKHSIQLSIEKAKIGKCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAASVRRGRCCCILHCTOTQVAQDCPS SSSVQRQRCESLQFQSLHTMSKKLVLNSVAGCADDALAGLVAACNP NLCLLQCHRVALRSLDLDSLGRVALLSGGGSCHEPAHAGFIGKG MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLIVKNTYGD RLNFGLAREQARAEGIPVEMVVIQDDSAFTVILKKAGRRGLCGTV LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSCSVPG SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMHDHMT NTTNASHVPVQPGSSVVMVNLLGGLSFLELGIJADATVRSLEG RGVKIARALVGTFMSALEMPGISITLILVDEPLLKLIDAETTAA AWPNVAAVSITGRKRSRVAAPAEQEPDSTAAGGSASKRMLAVL ERVCSTLLGLEEHLNALDRAAGGDGDCGTTHSRJARAJQEWLKEG PPPASPAOLLSKLSVLLLEKMGSSGALYGLFLTAAQPLKAKT SLFAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWSLFLIQVAFITLAVAAGGLYLYLAELIEEYTVATSRIIKYMIWFSTAVLIGLYVFERFTSMIGVGLFTNLVYFGLLQTFFIMLTSNPNFILSCGLVVVNHYLAFCQFAEEYYPFSEVLAYFTFCLWIIPFAFFVLSAGENVLPLPSTMQPQDDVVSNYFTKGKRGK
6763	2	760	SGPDFPPGRFRGCCRCCVRRPAGAGMELGGHWDMMNSAPRLVSETAERKQEQQKTCTEAEAADSGAVGARRFLCLYLGFLDLFGVSVMPVLLSLHVKSLSLGASPTVAGIVGSSYGILQLFSSLTVGCSDVVGRRSSLLACILSALSALGYLGAATNVFLFVLARVAGIFKHTLSISKALLSDDVVPEKERPLVIGHFNTIASGVGFIILGPVVGYYJTELEDGYYLTAFCFLVFLNAGLVWFFPRREAKPGSTE
6764	80	436	LKKMDTMWLSVRLFELQVRRVEILSEGNEQFOF1QIAKDFEDFRKKWQRTDHELGKYKDLLMKAETERSALDVKLKHARNQDVIEIKRRQRAEADCEKLERQIQLIREMLMCDSGSQ
6765	3	550	ARYSRVDFHFCRRRCRAVARAPRFLLQFPPSGPSRHFIAACVARWLRCGSVLSSEALSGSMSAMDGIVTEVAVGVKRGSDLELSGSVLSSPNSNMSSMVVTANGNDSKKFKGEDKMDGAPSRLVHLIRKLGEVTETEVIALGLPFGKVTLNMLKGKNAQFLELATEAAITNGNYSAVTPHLRNQ
6766	1	1287	EGGSFKAISLTWLWPLGEMKLHCEVEVISRHLPAIGLNRKGKVRAVSLCQQTTSRQPPVRAFLISTLKDKRGTRYELRENIEQFFTQFVDEGKATVRLKEPPVDICLSSKANSSLKCGFLSAMRLAHRGCNVDTPVSTLTPVKTSEFENFKTMVITSKKDYLPLSKGNFPYSLEHLQTSYCGLVRVDMRMILCKSLRKLDLSSHNIKKLPATIGDLIHLQELNNDNHLBESPVALCHSTLQKSLSLDSLSKNKNKALPVQFCQLQELKNLKLDDNNEIQLQPCKIGQJNLRFLSAARNKLPLPSEFRNLSLEYLDLFGNTFEPQPKVLPVJKLQAPLTLLESSARTILHNRIPYGSHIIPPHLCQDLDTAKICVCVGRFCLNSF1QGTTTMNLHSVAAHTVVVLVDNLGGTEAPIIISYFCSDLGCVNSSDI
6767	336	919	APMICLCSSDLQFRYKEAFLDRDGLCIGYCSVDDDRPMKHFLNGRLOSNDNEYKKDFAKSRQFHSSDQPGLLQAKRSQQLASDVHYRQPLPQPTCDPEOLGLRHAQKAHOLOSDVVKYKSDLNLTTRGVGWTPPGSYKVEMARAAELANARGLGLOGAYRGAAEAEAGDHSGEVNPDATETLHVKKKKALL
6768	2	363	PGSTISCYLLSEGSILPLCMQVACGEEKHRAPTMKTRARFKTELRLSPTDLGSCPPCGPCP,PKPAARGRRQSQDWGKSDERLLQAVENNDAPRAVAALIARKGLVPTKLDPEGKSAFH
6769	284	396	MSTPDFSTAENNOELANEWSCLKAMLTLMQAMQGQD
6770	1	397	DRNYQVIWSSTMKALHDYYKDEVVKKLMTFNYNSVMQVPRVEKITLNMGVGEIAADKKLKDAAADLAAISGQKPLITKARKSVAQFKIROGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLMATGKSVKDVRQAVLANLLEEDNKFACDQSKGPRWASWNIGVFCICRCAIGHRNGLVHISRVKSVNLDQWTOEQIQCMQEMGNGKANRILYEAYLPETFRRPQ1DYPYLFWSNLEG
6772	1	1400	AAAFLQGMTVNGFINTVITSLERRYDLHSYQSGLIASSYDIAACLCLTFVSYFGGSG/HKPRWLWGRVLMGTGSLVFAFLPHFTAGP*+GWKLDAGVRTCPANPR/PVCAG/HTSGLSRYQLVFMQLGQFLHGVGATPLYTLGVTYLDENVKSSCSP1YIAIFYTAAILGPAAGYLGCGGALN1YITEMGRRTLTTESPLWVGAWWVGFLGSGAAFFTAVPILGYPRQLPGSQRYAVMRAAEHMQLKDSSRGEASNPDFGKTIIDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLESQFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIKFCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLPEGHLNLTAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDGOKVYRDCSCIPONLSSGFCHATAGKCTST

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPQYHRQLYEKCTHKGRPGPOPWCATTPNFDQDRWGYCLEPKVKVDHCSKHSPCKGGTCVNMPSPGHCLCPQHJLTGNHCKEKECFPQQLLFFFHKNEIWYRTEQAAVARCQCKGPDAHCQRLASQACRTNPCLHGCRCLEVEGHRLCHCPVGYTGZPCDVGEG*GSGASRPRAPRWGDLAR
6774	146	389	LTELSDQQYFLFFILS/WVPTFLSMDVDGRRVIKADSFSKIISSGLRIGFLTGPKPLIERRVILHJQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLITARGGRRAPSPQLWTLVLALIEEKWRSRHLRMNSGRPETMENLPALYTIQFOGEVAMVTDYGFIAKIPGCRKQGLVHRTHMSSCRVDKPKSEIVDVGDKVWWXKLIGREMKNDRIKVSLSMKVNNQGTGKDLDPNNV/SLSKRGGGDPSRITLGRRSPRLS
6776	3	1108	HERHEGALQSQDALRISIPLDALSNNMRPEKCCRFTVHPWQQLHLNGLFPKTSADMEPCVGDGWVYDRISFSST1VTEWDLVCDSQLTSVAKFVFMAGMMVGGIILGGHLSDRFGRRFVLRWCYLOQVAIVGTCAAALAPTFIYCSLRLFLSGIAAMSLITNT1MLIAEWATHRFQAMGITLGMCPSGIAFMTLAGLAFIA RDWHILQLOVVSVPYFVIFLTSWLLESARWLIIINNKPEEGLKELRKAHHRSGMKNAVRDTLTLEILKSTMKKELEAAQKKKPFGLGERLHMPNICKRISLLPFTKFANFMAVYFLNLHG/LKHLGNVFLQLTFLGAV/TPPGQLVLHLGHWGSGRVSSRGVRVNCGLFVLIQVW
6777	779	63	CFFHGPAPWRDCEVRAFAKKOGOSGIISCIJAFSPAQPLVACGSYGRSLGLYAWDDGSPLALLGGHOGGITHLCFHPDGCRFFSGARKDAELLCWDLRLQSGGYPLWLSLGREVTTNQRIYFDLDPTGQFLVSGSTSGAVSVWDTDGPGNDCPKPEPVLSFLPQKDCCTNGVSLHPSLPLLGHCLPVSVCFLSPTESGGRRRGAGPGLSPRHRVHLECRCLQIWWCGGARLQH*+SPRARKGR
6778	311	805	IQSITDESGSIRRKNPANTRLFLNVP\ETETAGDSE\ERSPEEEVQADPRIRSKCPCTSPSPFKGRSPGEGET\DEPEKVFHHPGPDKSVAEKR\KGP\SPVSEEGI KDFFSMKPWEWENLNQSNVRRMH\T\AVRLNEIVVKKSRAKLVLLNMPGPPRNNGDENY
6779	2	535	RALRRQPRLLA\ANGI\EPESMAISEPIKGSRKPCVNKEEL\KKPMAKCAWKGPREPPQDARAEEAESPGGASESDQDGHESPPKKKAVAWVSAKNNPAPMRKKKVS LGPVSYVLLVDSEDGRKPVMPKKPGSRREASDQKAPRGQQPAEATASTSRGPKAKPECGSPRRATNESRKV
6780	3	403	HEVNDNPKPEIINILMSPGKEEISYIFEGFIDTFVALVRVQDKDSSGLNGEIVCKLHGHGFKLQKTYENNYLILTNATLDREKRSEYSLTVIAEDRGTPSLSTVKGHTFVQINDINDNPPHFQRSRYEFVISEK
6781	1	1269	AFTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVSINWAPSIPPVMSRPPVSSS1STPLPPNQITVFVTSNPIT'SANTSAALPTHOLASLMVTMPNACSKVMSEGOSAAOSNARPOFI TPVFINSSSI1QVMKGSQSPSTI PAAPLTITNSGLMPPSVAVVGPLHIPONIKFSSAPVPPNVALSSSPAPNIQITGRPLVLSRATPVQLPSPPCTSSPVPSHPPVQOVKELNPDEASPQVNTSADQNTLPSSQSTTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKACKKVTGSLEKGEEOYQGADGETEGQGLDTTAPGLMGTEOLSTELDSKTPTPPAPTLKMTSSPVPGPTASAGPSLPGGALPTSVRS:VTTLVPSELISAVPTTKSNEGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCL\HEDPQSPPPLPAEKPPIGNTFSTVSGKLSNVERTRNLESNHPGQTGGFVRVPPRPLPPRVNGKTIPTQQPPTKVPPERPPPPLSATRRSNKKLFPNRSSSDMDLQKKQSNLATGLSKAKSQVFKNQDPVLPFRPKPGHPLYSKMLSVPHGTANEDIVSQNPGEELSCKRGDVLVMLQTKETENNYLECQKGEDTGRVHLSQMKLITPLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DDLNLTSGEIVYLLKEIDTDWYRCNCRNCQIGIFPANYVKVIIDI PEGNGKRECVCSSHCVGSRCAVRFYIGEQKDELSFSEGEII IKEYVNEEWAKGEVRGRTGIFPLNVEPVEDYPTSGANVLSTKV PLTKKKEDSGNSQVNSLPAEWAELHSFTAETSDDLSFKRGDR I
6783	3	1750	SYHHHHAAQQS\AASPNLNTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRI\IAMVTAINSQKAVLSTDVQNTPVNLOTSSKV\I GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLLPRPNF LPQVRPKPVACNNIPIAPAPPMLAAPQLIQRPVMLTKFTPTTL PTSONSJHPV\VVNGQTATIAKTFPMAQLTSIVIA\TGTRLAGP QTVQLSKPSLE\OTVKSHTETDEKQTESRTITPPAAPPKKREEN PKQLAFMVSLC\I\VT\DH\HLEI\QS\KR\ER\KR\RTTANPVSGAVFE PERKKS\AVT\YLN\ST\H\PG\TR\K\RG\RP\K\Y\NA\VL\G\G\AL\T\PT\SP\Q\I SHPDSPENEKT\TT\TF\PA\VP\Q\VP\VS\LP\SP\T\SD\G\DI\H\ED\FC\VC RKSGOLLMCDTCSR\Y\H\LD\CL\DP\PL\K\T\PK\GM\W\I\CP\RC\Q\D\Q\ML\K KEEAI\WP\PG\T\LA\I\VS\H\Y\IA\Y\KA\KE\EE\K\Q\K\LL\K\W\SS\DL\K\Q\ER\EE\Q LEQKV\K\Q\LS\NS\I\SK\CM\EM\K\NT\I\LA\RK\Q\EM\H\SS\LE\K\V\K\Q\I\RL\I\H GIDLS\K\PV\DS\I\T\VG\A\I\SN\G\PD\CT\PP\A\AT\ST\T\PA\PS\SS\Q\SC\T ANCNQ\G\EE\K
6784	3	1750	SYHHHHAAQQS\AASPNLNTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRI\IAMVTAINSQKAVLSTDVQNTPVNLOTSSKV\I GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLLPRPNF LPQVRPKPVACNNIPIAPAPPMLAAPQLIQRPVMLTKFTPTTL PTSONSJHPV\VVNGQTATIAKTFPMAQLTSIVIA\TGTRLAGP QTVQLSKPSLE\OTVKSHTETDEKQTESRTITPPAAPPKKREEN PKQLAFMVSLC\I\VT\DH\HLEI\QS\KR\ER\KR\RTTANPVSGAVFE PERKKS\AVT\YLN\ST\H\PG\TR\K\RG\RP\K\Y\NA\VL\G\G\AL\T\PT\SP\Q\I SHPDSPENEKT\TT\TF\PA\VP\Q\VP\VS\LP\SP\T\SD\G\DI\H\ED\FC\VC RKSGOLLMCDTCSR\Y\H\LD\CL\DP\PL\K\T\PK\GM\W\I\CP\RC\Q\D\Q\ML\K KEEAI\WP\PG\T\LA\I\VS\H\Y\IA\Y\KA\KE\EE\K\Q\K\LL\K\W\SS\DL\K\Q\ER\EE\Q LEQKV\K\Q\LS\NS\I\SK\CM\EM\K\NT\I\LA\RK\Q\EM\H\SS\LE\K\V\K\Q\I\RL\I\H GIDLS\K\PV\DS\I\T\VG\A\I\SN\G\PD\CT\PP\A\AT\ST\T\PA\PS\SS\Q\SC\T ANCNQ\G\EE\K
6785	1	528	LGNTV\I\H\Y\CS\MS\K\PE\CL\K\LL\RS\K\PT\VD\I\VN\Q\AG\ET\AL\DI\AK\R LK\AT\Q\ED\LL\SC\A\K\SG\K\F\N\PH\H\Y\VE\W\N\LR\Q\EE\I\DE\SS\DD\LL\DD K\PS\VK\K\ER\SP\H\PO\SC\H\SS\I\SP\Q\K\LA\LP\G\F\ST\PR\K\Q\RL\SY GA\FT\N\Q\I\F\V\ST\T\DS\PT\SP\T\TE\A\PL\PP\RN\A\G\K\G\PT\G\PP\I\T\PH\I
6786	1826	1397	RSPKVLV\I\AP\T\EL\A\N\H\VS\RD\K\J\I\TR\K\LT\VA\RF\Y\G\CT\SY\Q\SC\Q I\N\H\TR\N\G\I\D\I\L\I\N\G\T\PG\I\K\DH\Q\CR\SL\DL\SK\LR\H\VV\I\DE\VD\Q\ML D\LG\FA\Q\VE\DI\I\H\ES\Y\K\T\D\SE\DN\Q\T\LL\FS\AT\CP\Q\W\Y\T\VA\K\K Y\M\K\SR\Y\Q\VD\I\I\G\K\MT\Q\K\AA\TT\B\H\LA\I\Q\CH\W\Q\R\PA\I\G\DV\I\Q V\Y\SG\G\EG\RA\I\I\PC\T\K\N\V\T\EM\A\N\PH\I\K\Q\N\A\Q\CL\H\G\DI\A\Q\SR E\I\T\K\G\F\REG\G\F\K\VL\VA\T\N\A\A\G\L\I\PE\I\VD\LV\I\Q\SS\PP\Q\DV\ES Y\I\H\RS\G\T\G\RA\G\T\G\I\G\I\CF\Y\Q\PR\G\Q\R\Y\VE\Q\K\A\G\I\T\K\RV\G V\P\ST\MD\LV\K\SK\I\MD\A\I\RS\LA\SV\Y\A\A\G\F\T\MT\I\LES\I\Q\DV\SC D\A\A\A\A\LA\H\I\G\A\SS\I\G\T\P\RS\I\LT\I\G\F\T\MT\I\LES\I\Q\DV\SC A\N\K\EL\N\K\L\SS\I\A\N\Q\I\T\RM\CL\K\LL\K\G\V\CF\DV\PT\T\ES\ER\I\Q\AE W\H\DS\W\I\LS\I\V\PA\K\I\PE\I\Y\Y\DG\N\T\SS\N\SR\G\W\SS\G\RS\G\RS\G\K\RS R\SG\G\RS\G\RS\G\K\RS\Q\G\RS\G\RS\Q\D\G\RR\RS\G\N\RN\RS\G\RS\G\H\K\RS FD\*V\Y\H\LV\DF\I\LS\DF\I\LV\DS\I\V\LT\G\R\Q\I\DH\LT\G\I\DH\LT\SH\I SV\W\N
6787	2646	2270	PSSFPKVN\PL\EE\PP\K\K\RS\G\G\SL\TP\K\Q\I\Q\N\G\P\*P\Q\T\FF\I F\EL\G\SP\G\G\VI\SA\I\CN\I\RL\LL\G\SS\I\DP\A\PA\PA\SR\VA\G\I\G\T\CH\H\A\W\I L\VF\I\VE\G\H\H\I\G\O\A\G\I\K\LL\T\I\I\H\PP\W\PP\K\VL\G\I\O\T
6788	16	936	GGTV\DL\I\DM\I\A\VS\I\LA\VR\GG\I\AT\VR\RV\RE\SN\I\H\E\K\SK\G\K\T R\EG\A\ED\K\MT\G\I\G\I\LS\I\N\R\K\M\Y\LL\K\T\A\F\PS\I\Q\I\N\T\EE\H\VD\I\EL\Q

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EVILWGS*DS*GYPXGK*LLPKEVPSR/RVLLSGLTPLDATQE\FTEDLSK\YVTIMVCVAVNGKPMILGVHKPFSEYTAWAMVDGGSNVKARSSYNEKTPRIVVRSRSHSGMVKQVALQTFGNQTTIIPAGGAGYKVVLALLDPDKSQEKADLYIHVTYIKKWDICAGNAILKALGGHMTTLSGEESIYTGSDEGEGGLASIRMNHQALVRKLPDLEKTGHK
6789	2	678	GNGINVLKTAPESAIKFMAYEIQIKRLVW**PGDS*GF/YERLVA GSLAGAIAOSSYIPMVEVLKTRMALKTGOYSGMILDCARRILARE GVAAFYKGYVPMNLGIIPYAGIDLAVYETLKNAWLOHYAVNSAD PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQSIEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVYENLKI TLGVQSR
6790	2	4068	APPAGRRRMOAAPRAGCGAALLLWIVSSCLCRAWTAPSTSOKCD EPLVSGLPHVAFSSSSISGSYSSPGYAKINKRGGAGGWPSDSD HYOWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW KPYHQDGNIWAFPGNINSDGVVRHELOHP1IARYVRIVPLDWN EGRIGLRIEVYGCYIWADVINFDGHVVLPYRFRNKKMKTLDV ALNFKTSESECVILHGEQCGQDYITLELKAKLVLISLNLSGSNQL GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRRSMQHFR TNGEFDYLDLDYEITFGGIPFSKGPKSSSR1KFKGCMESINYNG VNITDLARRKLEPSNVGNLSFSCVEPYTPVFFNATSYLEVPG RLNQDLFSVQFRWTWNPNGLLVPSHFADNLGNVEIDLTESKVG VHINITQTKMSQIDISGSGLNDGQWHEVRFLAKENFAILTIDG DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFOCC MQLIQVDDQQLVNLYEVAQRKPGSFANVSIDMC1IJDRCVPNHCE HGGKCSQTWDSFKCTDETGYSGATCHNSIYEPSECEAYKHLGQT SNYYWIDPDGSCPLGLPKVYCNMTEDKWVTVSHDLQMQTPVVG YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL NTPDGSPTWVVGKANEKHYWGGSGPGIOKCACC1ERNCTDPK YYCNCDAKYKQWRKDAGFLSYKDHPVSVQVVGDTDROGSEAKL SVGPLRCOGDRNYWNAASFNPNSPSYLLHFSTFQGETSADISFYFK TLTPWGVFLENMGKEDFIKLELKSAATEVSFSFDVGNGPVEIVVR SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL ELYISOLFVGAGGQGQFLGCIRSRLRNGVTLDEERAKVTSGFI SGCSGHCSTSYTNCENGKCLERYHGYSCDCSNTAYDGTFCNKD VGAFFEKGMLRYNFQAPATNDSSRVDNAPDQNSHPDLAQ EEIRFSSTTKAPCILLIYISSFTDFLAVLVKPTESLOIRYNLG GTREPYNIIDVDHRNMANGOPHSVNITRHEKTIFLKLDHYPVSY HLPSSSDTFLNSPKSLFLGKVIELTKIDQEIHKYNTPGFTGCLS RVQFNQIAPLKAALRQTNASAHVH1QGELVESNCASPLTLS SSATDPWHLDSASADFPYNPQGQAIJRCVUNRNSAIIGGVIA AVVIFTPLCTP\VL\*SR\HVSPIKGTLPIPNEAKGAGSRQK KPGRRPSMNNNDPPTSORPIDESKEWPHLRGGYIANG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPEL/PGW SAVV*SWLTAASTKVAIILLPQPLE*LGLOIAFMASLATHFSNO NSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFTFSMMKHEDV EEVYVYLMHNGNTVPSMYSYEMKGKSDTSSNHAVLKLAGDEVW LRMNGNGLHGDHQRFSTFAGFLLFETK
6792	33	1073	VRHTNWGVDMYLFSLGSESPKGAIIGHIVSTEKTILAVERNVLL PPLWNRTFSWGFDDFSCLGSGYSDKVLMTFENLAAGRCCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPGLRLRQALYGHQAV TCLAASVTFSLIVSGSODCTCILWDLDDHLTHVTRLPAAHREGISA ITISDVSGETIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPWADTSQIIITGSQDGMRVWVKT/VGCEDVCSWTASRG APGSASKPKRPQVGEPPGLESRAGR\HCFDREAQQNQP\PTAL AVSRNHTKLLVGDERGRIFCWSDG\*EERGSRGSGTTVPG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSITCAGTVSLGLDAEGQEVFVPPSAVLPMVAFNDLVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSVYIPEFIAANQSRADNLIPGSRAQQLEQIRRDIRDFRSSAGLDKVIVLWTANTERFCEVPGLNNDTAENLRLRTIELGLEVSPSTLFAVASILEGCAFLNGSPONTLPGALELAWQHRVFVGDDFKSGQTKVKSLVLDLIESGLKTMISIVSYNHLGNNDGENLSAPLCFRSKEVSKSNVVDDMVQSNPVLVYTPGEEDHCVVIKYVYVGDSKRALDEYTSELMCGGTNTLVLHNTCEDSLLAIPMILDLLALLTELCORVSCCTDMDEPQTPHPVLSLSSFLFKAPLVPPGSPVNVNALFRQRCIENILRACVGLPPONHMLLEHKMERPGPSLKKVGPVAATYPMILNKKGPVPAATNGCTGDANGHQLQEPPMPTT*GPGHTVSRFLFLPAAPHDPTLKAPTNKGRCHFSPPTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGRPSRPGVRRGRERAGGRGSHGARSCK\EPAPPAPAPPEDHPDEEMG*TIDIKSFLPKGEKTYTCRCLRFVGNLPTDITEEDFKRLPERYGEPESEVFINRDRGFGFIRLESRTLAEIAKAEILDGTILKSRPLRIRFATHGAALTVKNLSPPVSNELLEOAFSQFGPVEKAVVVVDGRATGKGFVFAAKPPARKALERCGDGAFLLTTTPRPIVEPMEOFIDEDGLPEKLMGKTCQYHKEKEQPPRFAQPGTFFEFYASRVLKALDEMEKQKREQVDRNIREAKEKLEAEMEAARHEHQLMLMRQDLRMRQEEELRRLREELRNQELQKRKQIQLRHEEEHRRREEEMIRHREOEELRROQEGFKPNYME NYVCHFLR
6795	1740	1010	GPRRQTQVRDIEHDSF*DWAQQETDCAQNSGERL*KGV/LENFTMSKSAVKISLDLSSNPCLCEQDQDLLNMVTALDTAMKRMDAFNCEKVNQIQTKVIEPLKKFGSVPNSLNMAVKRREQALQDYRRLQAKVEKYEKEKTPVLAKLHQAREELRPVREDFEAKNROLLEEMPRFYGSRLDYFOPSFESLIRAQVYYSEMHKIFGDLSHQLDQPGHSDERORERENAEKLSLSELRALSTVADD
6796	48	683	GKEIQIPPTIKLAWLFLGLE*PVGALGKGVVSF**SHVALGQLGWLTAVRVSWRWELCVSAQEVVVSQRSA**SSPSPVGACPSLNPPETSVCEGRDCWQR*LPRFLSALVGQPGCWPOGAPPERCV*FGRCKWHLCSQVLR*ERRRCCRCLPRFA*GWRRRHORLGLGIHPAPLGSTSPPHPEGNSQCCR*GWAAELRLPSSVVL*GKLG*
6797	1620	211	TERMTPSQPTRGESCTRPSMMLWTSTWRCLTCWAGMFM.SVVGVTLGPMAQGLLSSASGTTTEATWTRPTTHTLIRWWLLTASRVDPPERPPPPSDDLTLLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPSA*SRLLTHTVGGSPSAWRPRPTSRSVSTPVSSSTETTASGCLTWSSSPAPCPSSSSAPAHSEASCKTSLWGS CGGSGDGSACGSWNLSMAGTSCSSPAMCSFSRAPS*RSASRPRTRWATTSAASSWAPRRCWCWA*SAT*PSSTTTISSLPHCGWPCPASCASAAAALSSTWATASVAGSCWGPIM*SSAHSPWCLSACSRSSMGTCL*RSPP*SGASRAAAAWCGSSPSSTFTPSSASSTWCASSSSRSPPAPTPSSIPAAQORRASCRPTSHSARTAPPASSAAGAARPAAFSAAAEGTPRSIRCK
6798	3894	1696	STJSKESLESWLKATNPNPSRQEDWEIIGFCQINKELEG*VSALWQLRGSGLGRGTTMAKEGOPGSPLRSALECVLLVPO\POIAVRLLAHKIQSPQEWALQALTYLGDRVSEKVKTKVIELLYSWTMALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPPKNFVDFDEEKSLLKSKNPPDLQEAQNLKIKSMVREDEARIQKVTKRLHTLEEVNNNNVRLLSEMLLHYSQEDSSDGDRLEMKELFDQCENKRRTLFKLASETEDNDNSLQDILQASDNLRSVJNSYKTIIEGQVINGEVATLTLFDSEGNQCSNQGTLIDLAELDTNSLSSVLA PAPTFPSSGIPILPPPQAGSPRSPRSSSSQAEATLGPSSSTSNA SWLDEELLCLGLADPAPNVPKESAGNSQWHLLOREQSDLDFFSPRPCTAACGASDAPLQPSAPSSSSQAPLPPPFPAPVVPASVPAPSAGSSLFSTGVAPALAPKVEPAPVPGHGLALGNSALHJLDALDQLEEAKVTSGLVVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
			PLSFQSGSPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF RILFHFAKECPGGRPDVLVVVSMINTAPLPVKSVLQAAVPKS MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRRLRYK LTFALGEQLSTEVGEVDQFPVQEWNGL
6799	3894	1696	STISWESLESWLNAKATNPNSRQEDWEYIIGFCDOINKELEG*VS ALWGQLRGSGLGRGTTMAKEQGPSPRLSAECVLLVPQ\PQIA VRLLAHKIQSPEWEALQALTYLGDRVSEKVTKVIELLYSWTM ALPEEAKIKDAYHMLKROGIVQSDPPIPVDRTLIPSPPPRKPNP VFDDEEKSKLLAKLKSKNPDDLQEANKLIKSMVREDEARIQKV TKRLHTLLEEVNNNNVRLLSEMLHYSQEDSSDGDRLEMKELFDC ENKRRRTLFKLASETEDNDNSLQASDNLRSRVINSYKTIIEG QVINGEVATLTPDSEGNQCSNQGTLIDLAELDTNSLSSVIA PAPTPPSSGIPILPPPQASGPSPRSRSSSQAEATLGPSSTSNAL SWLDEELLCLGLADPAPNVPVKESAGNSQWLLQREQSDLDFFS PRPGTAAACGASDAPLQLQPSAPSSSSQAPLPPPFPAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSAIHHLDAL DQLLEEAKVTSGLVKPTTSPPLIPTTPARPLPFPSTGPGSPLFQ PLSFQSGSPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF RILFHFAKECPGGRPDVLVVVSMINTAPLPVKSVLQAAVPKS MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRRLRYK LTFALGEQLSTEVGEVDQFPVQEWNGL
6800	404	1646	RRSPSTGLSPVPCPSSPSLSDYSIPIWSLSSGTIAWATPGK*AG *PQAW*LGLAPAIIFI/GLTRGRKQNKKEKMAEGGSGDVDDAGDC SGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGRARARA RATRARRARAVQKRASPNSDDTIVLSPQELQKVLCLEVMSEKPYILE AALTAALGNNAAAYAFNRDIIRDLGGPLIVAKILNTRDPPIVKEKAL I VLNJNLSVNAEORRLKVYMNQVCDDTITSRINSSVOLAGLRL TNMTVTNEYQHMLANSISDFRRLFSAGNEETKLQVLKLLLNLAE NPAMTRELLRAQVPSVSLGSLFNNKENKEVILKLLVI FENINDN FKWEENEPTQNOFGEGGSILFFFLKEFQVCADKVLGIESHHDFLVK VKVGKFMALKLAEMHMPKSQE
6801	:	1755	SAEFPESQQAQVTMHDVDAESFEVILVDYCYTGRVSLSEANVERL YAASDMLQLEYVREACASFLARRLDLTNTCAILKFADAFGHRKL RSQAQSYIAQNFQKQLSHMGSIREEETLADLTIAQLIAVRLRDSLDR VESEQTVCVIAVQWLEAAPKERSGPSSAEVFKCVRWMHTEEDQD YLEGLLTKPIVKKYCLDVIAGALQMRYGDLLYKSLVPVPNSSSS /R*QQQLSCICSRKSTPETYVVCQGDGDLWTPORSLSRYDPPY SGDIYTMPSPLTSFARTKTVTSSAVCVSPDHDIYLAQPRKD LW VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYLGGGRDPITGVK LKEVECYSVQRNQWALVAPVPHSFYFELIVVONYLYAVNSKRM LCYDPSPHNMWLNCAASLKRSDFQEACVFNDIEYCICDIPVMKVNP PARGEWRRISNIPLDSETHNYQIVNHDQKLLITSTTPQWKKNR VTVYEYDTREDQWINGMLGLQFDGFIICLARVYPSCLEPG OSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDEVVWQ VAPORNAQDQQQGSL
6802	157	1341	ETFLFLFFFLLSKTPGKTAQMAHFVQGTSRMIAAESSTEHKECAEPSTRKNLMNSLEQKIRKCLEKQRKELLEVNQQWDQQFRSMKELYERKVAELKTKLDAAERFLSTREKDPHQQRQKDRDQRQREDDQRQLTRDRLOREEKEKERLNEELHELKEENKLKGKNTLANKEKEHYEC EIKRLNKALQDALNIKCSFSEDCLRKSVEFCHEEMRTEMEVLK QQVOIYEEDFKKERSDRERLNQEKEELCQINETSQSQLNRLNSQI KACOMEKEKLEKQLKQMYCPCPNCGLVFHLQDPWVPTGPGAVQ KOREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPVCCQAG/PR TPGLK*SSCLWLPKC*NRFILSKESPSVEVHTNRERQQATREG
6803	3	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYALDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KMIVEMLRTDLSYLCRSWRMTCGQPTITFFPISHSMLDEDGTSILNS SILAALRKMQDGYFGCARVQTGKLSFELTTSCCTHLSFMDDGPE GKLYSEDYDDNYYDLESQNMNDYDSTSHARCGDEVARYLDHLL AHTAHPHKLAPTSQKGLLDRFQAAVQTTCDLMSLVTAKAKELHVQ NVHMYLPTKLFOASRPSFNLLDSPHPRQENQVFSVRVEIHLPRD OSGEVDFKALVQLQKETSSLQEQADILYMLYTMKGPDWNTELYN ERSATVRELLTELYGVGEIRHWGLIRYISGILRKKVEALDEAC TDLLSHQKHLTVGLPPREKTIASAPLPYEALTQLIDEASEGDM SISILTOEIMVYLMAMRTQPGFAEMFRLRIGLIIQVMATELA HSLRCSAEEATEGLMNLSPSAMXNLHHLISLGKEFGVERK/SVR PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRLS 1SAESQSPGTSMPSSGSFPSAYDQQSSKDSRQGQWQRRRLDG ALNRPVPGFQKVWKLQKCHGLSVEGFVLPSSSTMREMPGEIK FSVHVES\VLNVLLRPEYRQLLVEA1VLVTMLADIEHSIGSII AVEKIVVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD SAPSGRFGITMYLS\RAA\ATYVQELFLP\HSICAMQ
6804	1	951	GSPGKKEEAKAKNESLCMENSSNSSSDEEETKAKMTPKKYN GLEEKRKSLRTTGFYSGFSEVAEKRKIKLNNNSDERLQNSRAKDR KDVWSSIQGOWPKKT1KELFSDSDTEAAASPPHPAPEEGVAEES LQTVAAEESCSPSVLEKPPPVNVDSPKPIEKTVEVNDRKAEP SSGSNFS\*1PLPYLHLNRLHQSL\*OKGSRQOSSVTVSEPLAPN QEEVRSIKSETDSTIEVDVAGELQDLQSE\*LASRF\*COCEL KQ\*SARTRTS\*KSLYRSEKSERCSGRRKFIKKAEKKP\*SNSGK QOKEGRHK
6805	1539	206	RQPDLYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL VPSPVLRILBDHTAFSTEKSA DIVI CDEECDS PESVNQQTQEEESP I E V H T A E D V P I A V E V H A I S E D Y D I E T E N N S S E S I Q D Q T D E E P P A K L C K I L D K S Q A L N V T A Q Q K W P L L R A N S S G L Y K C E L C E F N S K Y F S D L K Q H M I L K H K R T D S N C R V C K E S F S T N M L L I E H A K L H E E D F Y I C K Y C D Y K T V I F E N L S Q H J A D T H F S D H L Y W C E Q C D V Q F S S S E L Y L H F Q E H S C D E O Y L C O F C E H E T N D P E D L H S H V V N E H A C K L I E L S D K Y N N G E H G Q Y S L L S K I T F D K C K N F F C O V C G F R S R L H T N V N R H V A I E H T K I F P H V C D D C G K G F S S M L E \ I A G H L N S H L S E G I Y L C Q Y W E Y S T G Q I E D L K I H L D F K H S A D L P H K C S D C L M R F G N E R E L I S H L P V H E T T
6806	272	3794	VALCPNSDPVMFMDAFYGCCLLAEGLGPVIEVPLTRKDAGSQQV GFLLGSCGVFLALTIDACQKGLPKAQTGEVAFKGWPPLSWLV DGKHHLAKPPKDWHPLAQDTGTTGAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTOACGYSEATLTNVLDFKRDAGLWVHGVLTSVMNR MHVVSPVYALMKANPLSWIQKVCFYKARAALVKS1RDMHWSLLAQ RGQRDVSLSL\RM1IVADGANPWSISSCDAFLNVQSRGLRPEV 1CPCASPEALTVAIRRPPDLGCPPRKA\LSMNGLSYGVIRVD TEEKLSVLTQDVQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTA\YGLLGITKVNFEAVPVTGAP\IFDRPFTRTGLLG FIGPDHVF1VGKLDGLMVTGVRHNA\DDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQ\MSRV1QAI D SIH0VGVYCLALVPANTLPKA\LG\HISETKQR\LEGT1LHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMI\VGNLVAGKRIAQASGR ELAHLESDQARKFLFLADVLQWRAHTTPDHPFL\LLNAKGTVT STATCVQLHKAERVAALMEKGRLS\VGDHVALVYPPGVDLIAA FYGCLYCCGVPTVTPHPQNLGTTLPV\K\IVEVSKSACVLT QAVTRLLRSKEAAAADIRTWPTI\LDTDDIPKKKJASVFRPPSP DVLAYLDFSVSTTGJLLAGVKMSHAATSLCRS1K1QCELYPSRQ IAICLDPYCGLG\FAWLCLCSVYSGHQS\VLVPPLE\NSNVSLWLS AVS\QYKARVTFCCYSV\MEMCTKGLGAQ\TGVLRMKCVNLSCV RTCAVVAEERP\RIALTQFSKLFKDLGLPARAVSTTFGCRV NVAIC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LOGTAGDPPTTVYVDMRFLFDRVRLVERGSPHSPLMESGKIL PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTIVYGEAL HADHFSARLSFGDTQTIWARTGYLGFRLRTELTDASGGRHDALY VVGSLDETLERLGRMRYHPIDIETSVIRAHRSIAECAVFTWTNLL VVVVELGLEQDALDLVALVTNVVLEEHYLVVGVVIVDPGVIP INSGEKGORMHLRDGLADQLDPIYVAYNM
6807	1444	606	VGHDTVHJMTCFPKCLGFSPPVVTVSPRSEESHTTVSGGNG SVFOAGPQLQALNLEARRGS1GAALSSRDVSGLPVYAQSGEPR RLTQAQVAAPFGENALEHSSDQDTWDLSLRSPGFCSPLSGGGAE SLPPGGPGHAEAGHLGKVCDFHLNHQCPSPTSVLPTEVAAPPLE KILSVDSAVAVDCAYRTVPKPCPQPGPHCSLLTEGCLRSLSGDLN RFPGMEVHSGORELESVVAVGEAMA\LKFPGMAMSYCLRDRSR FLFLRPLMGLSCPLQVQ
6808	2063	737	GVGSGAASALARSPLASRLSSRRTRAPRSGAMORLAMDLRML SRELSLYLEHQVRVGFSGVGVLSSLLICPSVAYAFYYLSSI PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\ ITSKPPVQYRNELIKTADGQ1ISLDWFNDNSTCYMDASTRPTI LLPGGLTGTCSKESYILHHMIIHLSEELGYRCVVFNRRGVAGENLLT PRTYCCANTEDEDLTIVHHVHSLYPSAPFLAAGVSMGGMILLNYL GKIGSKTPLMAAATFSVGWTIFACSESLEKPLNWLFLNYLITC LQSSVNKHRRHMFKVQVMDHVMKAKSIREFDKRTFTSVMFGYQTI DDYYTDAEPSPRLKSVG1PVLCLNSVDDVFSPSHAIPETAKQN PNVALVLTSYGGHIGFLEG1WPRQSTYMDRVFKQFVQAMVEHGH ELS
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTOPIAGTQTVPO TDEAAQTDSQPLHPSDPTEKQQPKR1HVSNI1PFRFRDPD1RQMF GQFGKILDVEII1FNERGSKGFVFTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMNTKKTGNPYTNGWKLNPVVGAVYGP VTGFPYPTTGTAVAYRGAH1LRRGRGRAVNTFRAAPPPP1PTY AVVYQDGFYGAET\LEATQPTD1SPLQRQPTATVTAESTQLP TRT1TPSGPRRPTALEPCETFHRFLLG
6810	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTOPIAGTQTVPO TDEAAQTDSQPLHPSDPTEKQQPKR1HVSNI1PFRFRDPD1RQMF GQFGKILDVEII1FNERGSKGFVFTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMNTKKTGNPYTNGWKLNPVVGAVYGP VTGFPYPTTGTAVAYRGAH1LRRGRGRAVNTFRAAPPPP1PTY AVVYQDGFYGAET\LEATQPTD1SPLQRQPTATVTAESTQLP TRT1TPSGPRRPTALEPCETFHRFLLG
6811	1522	658	DLTVWVFVDCRVIASTHGH\KSWVSVVAFDPYTTSVVEGDPME FSGSDEDFODLHFGDRADSTOCRLSRRNSTDSPVSVTYRFG SVGQDQTLCLWDLTEDR1LPHOPLSRAHTHNV\NATSPAGSN GNSVTTGNSVPPPLPRSNSLPHSAVNAGSKSSVMGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLT TDPAKT1LGTPLCPRMEDVPLLEPLICKKIAHERLTVL1FLED CI1TACOEGFIC1TWRGPVGVVFSNP
6812	4001	1682	EDAVFS1LDLSTII1QGTWPLNGEELKSNPEGQVEPGALYRIEQ KGLQHRL1HAKHQDGSALVGFCSPGVQD5AALTIQESPVHIL SPQDKVSLTFTT1SERVVLTC1S1RVD1F1PATWYKDGQKVEESELL VVKMDGRKHRL1LPEAKVQD5GEFECRTEGVSAFFGVTVQDPPV HIVDPREHFVHAITSECVM1ACEV\DR\EDAPVRYKDGQEV ESDFVVL1ENEGPHRRLVLPATQFSDGGEFOCVA1GDECAYPTV TDVSSWIVYPSGVYVA1VRLERVV1LTC1CRPWA1VRWT EVVESPA1L1QKEDTVRRLVLPAVQ1EDSGEY1CE1D EVVTEPPVRI1YPRDEVTL1AVTLECVVLMCELS1REDAPV R1WYK DGL1VEESEALVLERDGP1CR1L1VLPAAQ1EDGGEFVCDAG DDSA FFT1VTEPPVQFLAETTPS1PLCVAPGEPVV1S1CELS1RAG APV



SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DGGE/LHS/ATTEHKP/VQATPVNL\TILTSTWQARLPOI
6819	1	961	GIPCTEMGNFDANVTIEIEFAIHYCFKTHSLEICIKACKNLAY GEEKKKKCNPYVKTYLLPDRSSQGRKRTGVQRNTVDPFQETLK YQVAPAQOLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS TTQSFRWHPRLRAKADKYEDSVQPSNGELTVRAKLVLPSPRKRLO EAQEGTIDOPSLHGCOLCLVVLGAKNLPVVRPGTILNSFVKGCLTL DQQLRLKSPVLRKQACPQWKHSFVSGVTPAQLRQSSLELTW DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSOSKLQWOKVLSS PNLWTDMLVLH
6820	1014	340	GDMVYJVGHPVPGFFEKTQNKAWFREGFNEKYLKVVVKHHRVIA GQFFGHETHTDSFRMLYDDAGVPISAMFITPGVTPWKTLPGVVN GANNPAIRVFYEDRATLSLKDMDVTFYFMNLQANAOGTPRWELEY QLTEAYGVFDASAHSMHTVLDRIAGDOSTLQRYVVYNSVSYAG VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVQLPLLLMAL LGLCT
6821	1088	516	EFDIYR/EGGEGFPVTRDDSSNGFPRTQHGPSPVHPIQSPQN RFCVLTLDPETLPAIATTIIDLVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECIVQAQPLAADIISAYYISTFNFHALVPEDEGI GSVIEVLQRQEGLAS
6822	1088	516	EFDIYR/EGGEGFPVTRDDSSNGFPRTQHGPSPVHPIQSPQN RFCVLTLDPETLPAIATTIIDLVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECIVQAQPLAADIISAYYISTFNFHALVPEDEGI GSVIEVLQRQEGLAS
6823	654	221	PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGWPWRSVQTAC GIPQQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRGKVIALNPLL
6824	858	104	LLLAQRWGWC\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG LLPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWT NWRFLPEALFLHRAFHALLTAAHTLTLFLALCRNRTGESILS LLRDPSKRVKVPPPOPLTPNQIVSTLFTSNFIGICFCSRSLHYQFYV WYFHTLPLWAMPARWLTHLLRLIVLGLIELSNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGIQLASDWTISDTGWILLIILCSLMEPWALGACTFVHL PKFDPLVILKTLSSYPPIKSMMGAPIVYRMLLQQDLSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPFGTEGDIJIRVKPIRPI GIFSGYVNDPKTAANIRGDFWLLGDRGKIKDEDGYQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKA VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPKRIEFVNLPK TVTGK1QRA\KLRDKEWKMSGKAPCAVRLRDIHLDPLLSLSF PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFPKW/VNIALAFELLGERASPNSFWQPYIQLTPREYDTP LYFEEDERYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPH NKLPLKDSFTYEDYRWA VSSVMTRQNQIPTEDGSRTLALIPLW DMCNHTNGLITTCYNEEDDRCEVALQDFRAGEQIYIFYGTRSN AEFVIHSGFFFDDNSHDRVKI KLGVSKSDRLYAMKAEVLARAGI PTSSVFAHFTEPPI SACAQLLAFLRVFCMTEEELKEHLLGEAID RIFTLGNSEFPVSDNEVKLWTFLEDRASLLLKTYKTTIEEDKS VLIKHDLSVRAKMAIKLRLGEKILEKAVKSAAVNREYYRQOME EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI REAISKAKATENGVLNGENSI PNGTRSENESLNQESKRAVEDAK GSSSDSTAGVKE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6827	1	779	SSVVEFGLSVLGGFLFLFVLENMLGLLRRHGLRPRCCRRKRRNL ETRNLDPENGSMALCPLQAAPEPGAQGOREKNSCHPPALAPPG HQGHSHGHQGGTDITMVLGDLHNLTDGLAIGAAFSDGFSSG LSTTLAVFCHELPELGDFAMLLQSGLSFRRLLLSLVSGALCL GGAVLGVLGLSLGPVPLTPWVFGVTAGVFLYVALVMLPALFPSS GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
6828	3	1654	KSQHG\WLOLHMHSCKEGYVKDLKGNGPLHRAMLLDNGTRFSE LGHLSCTASLKRCCSFSQSGRDDTWRYKTPHRVAFVEKLTKLVL QLPNFWKLWISYVNGSLFSETAEKSGQJERSKVRQRONDFKKM IQEVHMHSLVKLTRGALPLSIRDGEAKQYGGWEVKCELSGQWLA HAIQTVRLTHTESLTALIIPNDLQLTQDLIIDLRLRVCVMATLQH TAEZIKRLAEKEDWIVDNEGLTSLPCQFECQICIVCQLQSLKGVL CKPGEASVFOQPKTOEVEVQCLSINIMQFIYCLEQSLSTKPDADI DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT FLNIAEHPEK\HNFQG\EKITQVSMASLKELDQRLFENYIELKAD PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNI\AV\HAEV FTISKELVPRVLSKV\EA\SEELSRLMQCVSSFSKNGALQARL ICALRDTAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN KFKSSMHJQLTCFQAASSTMMKT
6829	1	782	MRMEEAGEAAPPAGAGGKGWVRLNVGGTVFLTRQTLCR EQKSFLSRLCOGEELQSDRDET\GAYLIDRDPTYFGPILNFLRHG KLVLQDKDMAEEGVLEAAEFYNIQPLIRI\KDRMEEKDYTVTQVP PKHVVYRVLQCQEEELTQMVTMSDGWRFEQLVNIGSSYNYGSED QAEFLCVSKELHSTPGLNGLESSRKTKSTEEOLEOOQOEEEV EEVEVEQVQEADAOEK\CCYKPEAPGCEAPDH\QLGVPV
6830	1	935	M\EPGSVNLISIVYRSRDFLVVNNKHWDRVJDSKA\RETTLIQL RYRFP\ELADPDTCYGFRFC\HQLDFSTSGALCVALNKAAGSAYR CFKERRVT\KAYLALLR\GHIQESRVTISHAIGRNSTEGRAJITMC EGSOGCENPKPSLTD\LLVLEI\GLYAGD\GPKV\LLKPLTGRTHOL RV\HCSALGH\PPVGDLYGEVSGREDRPF\RMMLHAFY\LR\IPTDT ECVEVCTPDPFLPSLD\CN\SPHTL\LOS\LG\LVQ\LR\ATPDPDPE DRGPRPGSPS\LLPGPGRPPPPTKPP\TEAORGPC\OL\SEWT LEPDS
6831	3	1087	SLFFGSSTPDNKVAE\OEDLETQPSPSVEKAVTV\IDPEGT\PTNF NVAEK\PA\DHSL\SEV\KLT\TADE\PRGTV\KSGDGQN\KEKSMILSN VEDLQQPKFISEV\SE\DYGKKEISGDSEEMN\INSV\TSADGENL EIQSYSLIGE\KLV\ME\AKTIVP\HVT\DSKRVQ\KPAIAPP\SKWNI SIFKEEPRS\DKQK\SL\SF\DV\DKV\PQ\QPKS\ASS\NFASK\NITKE SEKPE\I\LPV\EE\KGS\SL\DF\SE\DR\KKEM\QNP\TSL\K\I\SE\ETK LRSV\SPTE\KK\EN\LR\SY\TL\A\EK\VL\A\EK\K\N\SV\A\PL\LR\DS NE\J\GK\T\Q\IT\LG\SR\ST\EL\KES\KA\DA\MP\Q\H\Y\Q\N\ED\Y\N\ER\PK\I\IVG SEKE\KDE\KKKK
6832	1809	412	MGSG\LS\GPP\QDN\SGE\AL\KE\PER\A\Q\H\SL\PN\FA\GG\Q\H\FF\Y\LL\VV VSLKKR\SE\DD\Y\EP\I\I\Y\Q\FP\K\RE\N\LL\R\K\I\PL\F CF\PD\G\N\W\A\SL\T\EP\Y\PRE\T\FS\FL\N\VG\SR\K\I\G\Y\CR\LL\PA\G\PG P\RL\PK\Y\CI\I\SC\I\G\CF\GL\FS\K\I\LD\VE\K\H\O\I\SM\A\Y\I\Y\PM\Q\GL R\EA\A\FP\A\PG\K\T\VL\K\SF\I\PD\G\T\EP\I\SL\T\RP\LD\SH\LE\H\VF\SSL L\H\CL\SL\SE\Q\I\LO\I\FA\SV\LE\K\I\FL\A\E\GL\SL\T\LS\Q\I\H\AAA\LL\Y P\FS\W\A\H\T\Y\I\P\VV\PE\SL\I\AT\VC\CP\T\PM\VG\VG\Q\M\RF\Q\EV\MD\SP\ME EV\LL\VN\LC\EG\T\FL\MS\VG\DE\K\I\LP\PL\Q\DD\I\LD\SL\G\Q\G\I\N\EL\KT A\Q\I\N\E\H\VG\G\P\Y\Q\FF\VK\I\VG\H\Y\A\Y\I\K\RE\A\N\Q\G\H\Q\F\Q\ER\SF\CK A\LT\SK\T\N\RF\Y\K\K\T\Q\I\FL\SL\I\Q\EA\K\SK\N\PP\A\G\Y\FO\OK\I\LE\Y Y\EE\Q\KK\Q\T\ET\K\G\K\N\CE\I\RA\VV\N\K\ND
6833	1	1129	PLMTL\SC\GG\I\PG\H\G\H\SH\GG\H\G\H\G\H\G\LP\K\G\PR\VK\STR\G\SS\DI\N V\A\PG\O\CP\Q\DE\ET\NT\LV\A\NT\NS\N\GL\K\LD\PA\DP\EN\PR\G\DT\VE\W Q\N\G\N\LV\RE\PD\H\ME\LE\ED\RA\G\Q\LN\MR\G\FL\H\VL\G\AL\G\SV\I\VV\VV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NALVFYFWKGCGEDFCVNPCKAFVETINSTHASVYEA GCPWVLYLDPTLCVVMVCILLYTTYPLLKESALIILQTVPKQID IRNLIKELRNVEGVEEVHHLVWOLAGSR1IATAH1KCEDPTSY MEVAKTIKDVFHNGH1HATTIQPEFASVGSKSSVPCELCRTQ CALKQCCGTLQPAQSGKDAAKTPAVSISCLELSNNLEKKPRRTK AENIPA\VVIEKN\IPNK\QPESSL
6834	76	1151	AGQERPAPIWRLWLPPTPSVSRKAEPAH1F1N1R*GA*E*RGGLP LCGSSASAYGHH*RLTPWSPGGS*HM*SSKAPVTCAREVVLVAGP CSKLVLSGARGIVGTTVQVLVE*QOPLL1FTGVWGLNLRAGEEE SRAL*1JEEVTQVRDAH1GNANVGCAQCLSQGVGSALAKALLE AAAARVRCCKEVLTSGDKQOAEVSVRL*VRDVCVVEAGCVEFGQ AHGRPGALAKGRGGTNEVEEQVQVVDGVQKLVLVSAHECHELVAG QDGEDQAAARTRLLQAGAHSAHGRQGQAPCRPHQEAGVSCH LQVVGDAL*ARE*APQ1IVL1LLEDVAOLRTGKKA*DLVVVDVE QLLQL
6835	3	834	G1PAADR\EASLELIKLDISRTFPNLC1FQQGGPVHDM1H51LG AYTCYRPDVGVQGMSFTAAL11LNLDTADAFIAFSNLLNKPQO MAFFRVDHGMLTYFAA1FVFFEENLPKLFAHF1KNNLTPD1Y IDW1FTLYSKSLPLD1LACR1WDVFCRDGEFLFR1ALG1KLKF D1LTKMDF1HMAQFLTRLPEDLP1PAEELPASIATI1QMSRNKKWA QV1TALQKDSREMREGKSVPTTLRLQREFALGTNCSPMPRPLCC FRLTPGQPRRTDAL
6836	3	850	MSCGRPPPDVDMG1T1KV\DNLT1RTSPDSLRRVFEKYGRVGDV Y1P1REH1TKAPRGFAFVFRH1DRRAQDAEAMDGAE1DGREL1RV QVARYGRRDLPRSRQGRRHAAGPEA/RYGRRSRSYGRRSRSPR RRHRSRERGPSCSRSRSSRYSRYSRSPY1SRYSRYSRYSR PY1SRYSRYSRYSRYSRYSRYSRYSRYSRYSRYSRYSRYSR SRSASTSKSSSARRSKSSSSVSRSRSSR1R1SSMTRSP1PRVSKRKS KSR1SR1RPPKSP1EEQGMSS
6837	2	1369	TDGA1AVGNPGPSD1YFPGTAP/GC1P1TRRF\SGTSSSGSKASGP PNPPA1QGDGT1SLSPNT1LESTSG1NDGKPVSGGGGRGR1RK1D1S GHVSPGT1FFDKYSAAPD1SGGAPGV1S PGQ1Q1ASGA1VGGSS1AGET RGAP1PHEKAL1TSPW1GK1GA1LL1CDQ1PDL1G1SL1DVG1AK1SD1SS PNVGEFASDEV1TSY1AN1DEV1SSSD1NP1Q1LV1K1AS1R1S1PL1V1G1P K1L1P1R1VG1A1G1E1H1G1P1K1A1P1P1G1C1M1S1N1T1P1D1S1P1D1 P1G1T1P1G1L1K1G1K1G1C1A1V1G1A1G1Q1D1S1H1D1S1A1M1S1T1 EDQ1P1G1L1K1G1K1G1C1A1V1G1A1G1Q1D1S1H1D1S1A1M1S1T1 D1D1S1M1A1H1S1A1W1Y1M1P1D1K1A1V1D1S1A1D1D1K1T1L1A1P1W1 K1A1H1D1P1A1K1A1S1Q1P1G1S1H1Q1L1Q1C1S1V1H1C1V1T1D1 S1K1S1D1S1N1R1F1T1V1A1L1T1
6838	16	499	LTDT1PP1PK1TH1H1S1ISD1Y1K1A1L1C1W1G1F1P1M1E1I1L1W1Q1D1E1E1 D1Q1T1R1M1E1L1V1E1T1R1P1A1G1D1G1T1F1Q1K1W1A1V1V1V1P1G1S1E1E1 G1L1P1E1L1R1W1Q1S1Q1S1P1T1I1P1V1G1V1A1G1V1L1G1A1V1V1T1G1V1A1V1M1C1 R1K1N1S1D1R1V1R1S1Y1S1A1S1A1S1Q1G1S1D1H1A1Q1G1S1D1V1S1T1A1C1 K1A1H1D1P1A1K1A1S1Q1P1G1S1H1Q1L1Q1C1S1V1H1C1V1T1D1
6839	3	1195	AAPAGGGPDP1E1A1S1F1G1R1H1L1S1W1P1Q1V1K1R1D1A1L1S1E1P1I1H1 R1G1N1F1P1T1L1S1V1Q1P1R1A1G1C1G1P1Q1H1G1C1A1S1H1V1L1 H1P1E1S1G1L1G1K1G1K1G1C1A1V1G1A1G1Q1D1S1H1D1S1A1M1S1T1 S1R1A1K1T1L1K1E1A1Y1V1Q1K1L1V1K1V1C1T1D1S1R1W1S1L1S1N1S1G1K1N1V1E1K1 F1V1D1S1V1R1Q1F1E1S1D1S1F1Q1I1D1S1L1F1G1Q1C1S1T1P1M1S1E1A1F1P1T1V1G1 E1S1Y1G1D1F1T1E1A1L1H1R1R1V1A1T1R1S1P1E1I1R1G1G1L1K1Y1C1H1L1V1R1G1F1R1 P1R1F1D1V1R1A1Q1Y1M1C1S1R1F1D1F1P1D1L1V1E1Q1R1T1L1E1Y1A1H1F1G1A1D1 A1A1R1Y1A1C1V1L1H1R1V1V1E1S1T1V1C1L1M1H1E1R1Q1R1T1L1D1I1A1A1L1Q1A1E1 Q1G1P1A1A1L1W1R1P1P1G1V1V1P1A1T1V1N1Y1V1T1P1V1Q1P1L1A1H1A1Y1P1T1W1P1 C1N1
6840	4254	2061	E1Q1G1F1S1V1P1D1V1P1K1S1M1A1C1E1N1S1C1I1V1G1F1K1D1Y1Y1L1R1V1D1G1K1G1S1K1E1L1 F1P1T1G1K1Q1L1P1V1A1P1A1L1D1G1K1V1A1V1G1Q1D1Q1D1L1T1V1V1N1E1E1G1C1I1C1T1Q1K1C1A1L1N1W1

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TDIPVAMEHQPPIIAVLPKVVEIRTFEPKLLVQSIELQRPRFI TSGGSNIIYVASNHFWVRLIIPVPMATQIQQQLQDKQFELALQLA EMKDDDSDEKQQQIHHIKNLYAFNLFQOKRFDQSMQVFAKLGTD PTHVMGLYPDILLPTDYRKQLQYPNPLFVLSGABEKAHLALIDY LTKRSQQLVKKLNDSDHQSSSTSPMLEGFTIKSKKKLQLIDTT LLKCYLHTNVNALVALPVLRLLENNHCHIEESEHVLKAAHKYSELII LYEKKGHLHEKALQVLVDQSKKUNSPLKCHERTVOYQLQHLCTENL HLJFSYSVWVLRDFPEDGLKIPTEDLPEVESLPRDRVLGLFIEN FKGLAIPIYLEHHIHWWEETGSRFHNCIOLYCEKVQGLMKEYLL SFFAGKTPVPAGEEEEGELGEYRQKLLMFLIESYYDPGRLICDF PFDGILLEERALLGRMGKHEQALFIYVHILKDTMAEEYCHKHY DRVKDGKNDVYLSLLRMYLSFPSIHLGP:KLELLEPKANLQAA LQVLELHHSKLDTTKALNLLFANTQINDIRIFLEKVLEENAOKK RFNOVLKNNLHAEFLRV\QEEERLHQOVKCIITEEKVCMVCKKK IGNSAFARYPNGVVVHFC\KEVNPA
6841	1	3206	TPTSTTGTNSNTPSSVPSAATPLNESLQPLGDYGVGSKNSKRA REKRDSDRNMEVQVTOEMRNVSJGMGSSDEWSDVQDIIIDSTPELD MCPETRLDRGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD VDFGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA KVDOLSGEQEVLRGELEAAKQAKVLENRKELEELKRVKSEA IIAARREPKEEADVSSYLCTESDKIPMACRRRFTRVEMARVLME RNQYKERLMEQEA VRWTE MIRASREHPSVQEKKKSTI WQFFSR LFS SSSSSPPPAKRYPYPSGNIHYSKPTTAGFSQRRRNHAMCPISAG SRPLFFPDDDCTS S ARREQYRQVREHVRNDGRLQACGW SLPAKYKOLSPNGGQEDTRMKNVPVPUVYCFPLVEKDPTMKLWCA AGVNLSGWRPNEDDAGNGVVKPAPGRDPLTCREGDGEPKSAHTS PEKKKAKELPEMDATSSRVWILTSTLITSKVVIIDANQPGTVVD QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV LAGI TLVGCATRCNPRSNCSERGDTPVLEKGQGEVATIANGKV NPSOSTEEATEATEVFPDPGPSEPE TATLRPGPLTEHVFTDPA PSSG P OPGSENGFEPDSSSTRPEPEPSGDPTGAGSSAAPT MWLG AONCVLYVHSAVANWKCLHSIJKLDSVLSLVHVKGRLVVALAD GTLA JFHRGEDGQWDLNSYHLMQDGHPHHSIRCMAMVVYDRVWC YKNUVHIVIOPKTMQIEKSFDAPRRESQVRQLA WIGDGVVWSIR LDSTLRLYHAHTHQILODVIDE PYVSXWMLGTGLGSFVRITAL LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP TSGEG\ARPGG\I HVY G\DDSSDRAARSFI\YCSMAQOLCFH GHRDAVKKFFVSVPGNVLA TNGSVLDSPAEGPGPAAPASEVEGQ KLRMVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVL SKA ERSH\I WVOVSYTPE
6842	3	926	RCOOLSATILTDHQYLERTPLCAILKQKAPQYRIRAKLRSYKP RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN TSLVDSK IWTTKNQKGRKVAVHFWVKNNGILPLSNECLLJEGGT LSEI C KLSNKPNSVI PVRSGHEDLELLDLSAPFLI QGTVHHYGC KQWST* RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVVFMTFT LDDCTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC PPG I KIDAYPWLECFIKSYNVTNGTDNQ1CYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRJHTGERPYECSE CGRSPAE NSSLIKHRLVHTGERPYECVECGKSFRRSSSLHQQR VHTRERPYECSECGKSFSLRSNLIHHORVHTGERHECGQCGKSF SRKSSLI IHLRVHTGERPYECSDCGKSF AENSSLIKHRLVHTGE R PYECIDCGKSF RHSSFRHQRVHTGMRPYK*SKFWKESCPGF LLOLOGORVHTGSRCYECDKWG IFFS*NASFFT*KSAPTEEVPFE CNECEKAFSPSLSVTTIFT
6844	244	642	EHOLJAGFELRKTOTSMSLGT TREKTRVKSTAYLSPOELEDVY QYDVKSEIYSGFIVLWEIATGDI PFOGCNSEKIRKLVAVKRQQE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLGEDCFSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK J
6845	3	1519	VAVRDECYWRHVFWDQDLMWMLLFIIMCHPETARARLEYRIRTLD GALENAQNLYGQGAKPAWESADSGLEVCPCEDIYGVQEYHVNAGAV GLAFELYYHTTQDLQLFREAGGWDVRAVAEFWCSKREVEWSPREE KYHLRGVMSPDEYHSGVNNSYTNTVVLVONSLRFAAALAQDLGLP IPSQWLAVALDKIKVDPVDEQNFHPEFDGYEPGEVVKQADVVLLG YPVPFSLSPDVRRKNLIEIYEAVTSPQGPAMTWMSMFAVGWMELKD AVRARGILLDRSFANMAEPFKVWTENADGSGAVNFTLGMGGFLQA VVFGCTGFRVTRAGVTDFPVCLSGISRVSVSGIFYCGNKLNFSE SEDSVTVEVTARAGPHWPHLEAEIWPQSRLSLLPGHKVSPRS AGRIQMSPKLPGSSSEFPGKTFSDVDRDPLQSPVILWVTLGSSSP TESLTVDIPASE*SGTGASETSLGPSLWFRLHPPLGTLACHPS PAARLSGKVHAAWPEFKAFCL
6846	213	1256	LYFLKTIK*LNRLAEPH*YENEKLTKLRLNTIMEQYTRTEESARG IIFTKTRQSAVLSQWITENEKFAEVGVKAHHLIGAGHSSEFKP MTONEQKEV1SKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL VTNEIAMVQARGRARADESTYLVLAHSGSGVIEHETVNDFREKM MYKAIHCVCQNMKPEEYAHKILELQMQSIMEKKMKTKRN1AKHYK NNPSLITFLCKNCVLAQCSGEDIHVIEKMHVNMTPEFKELYIV RENKTLQKKCADYQINGEIICKCGQAWGTMVMHKGLDPLCPLKIR KFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLLEMLPLDILALILYPPSYVVPYTCIHSDDSLSRKYCLT WFEDALGVL*RAEAJQPHCVNAGDRMEKFQRQKYWNKLOTLRQQ PFAYGTLTCSRLLDTREHCLNEFNFPDPYPSKVKQRENGVALRCF FCVVRSLALGWEERQALAVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLLIVAE RIAGMDPVVHSALREERLLLVOTGSSPCLDLSRLDKGLAALVR ERGADLVIIEGMGRAVHTNYHAIRCESLKLAVIKNAWLAERLG GRLFSVIKYEVPAE
6848	19	16	AMWWNSLDGIERNIVLSPNPKRNTLSSLAMLKSLSQSDILHADSDND LKVIISIAEGPVFSSQHDLKELTEEQGRDYHAEVFQTC SKVMMH IRNHPPVIAVMVNGLATAAGCOLVASCSDIAVASDKSSPATPGVN VGLFCSTPGVALARAVPRKVALEMIFTGEPISAQEALLHGLLNK VVEPEAELQEETMRIAISLSPVSLGKATFYKQLPQDLGTA YLTLSQAMVDNLALRDQEGITAFLQKRPVWSHEPV*VEH
6849	70	821	SLGVGDGSCLEQGSPAPRPQTDSP*PVGNWATQQEDLYHQS YEC VCVLFASVPDFKEFYSESINHEGLEYCLRLNNEIIADFDDELLSK PKFSGVKEIKTIGSTYMAATGLNATSGODAQDAAERSCSH LGTM VFAVALGSKLDVINKHSFNNFRLRVCLNQGPVVAQVJGAQKQ YDIWGNTRVNVASRMESTGVLGKIQVTEAWALQSLGTYCYSRG VIKVKGKGQLCTYFLNTDLTRGPPSATLG
6850	2	1235	ARGLNHETWTFEKLQRHISRNAQDKQELHLFMLS GVPDAVFDLTD LDVILKLELIPEAKI PAKISOMTNLQELHLCHCPAKVEQTA FSL RDHLRCLHVFKFTDVAEIPAWVLLKLNRLRELYLIGNLNSENNKMI GLESLERLRHLKILHVKSNLTKVPSNITDVAHPLTKLVIHNDGT KLLVVLNSLKKMMNVAEELQNCLELRIPHAIFSLSNLQELDLKS NNIRTIEIIISFOHLKRLTCLKLWHNKIVTIPPSITHVKNLES YFSNNKLESPLPVAVFSLQKLRLCDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKC1KLRTLN LGONCITSLPEKVGQLSQ LTOLELKGNCLDRLPQOLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTD LRDLFNFNQVEQGPILLSCPKAGTDLSMGRAREVGWMAGLM1GAGA CYCVYKLTIGRDDSEKLEEEGEEWDDQELDEEEDPDIWFDFT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MARPTWEDGDWTEPGAGPGGTEDRPGGGKANRAHPIKQKPFPPYE HKNTWSAQNCNKNGSCVLDLSKCLFIQKLLFAEPKDAQGFPFSQD INSHLASLSMARNTSPDPPTVREALCAPDNLNASIESOGQIKM YINEVCRRETCSRCCNSFLQQAGLNLLISMIVNNMLAKSASDLK FPLISEGSGCAKVQVLKPLMLGSEKPVLAGELVGAQMLFSFMSL FIRGNREILLETPA
6852	1	407	RTRGEETTYKHNQKNIYAAARTPATLFAVMFAMYIISGLT GFIGLNSIAVLCNLVMGLALIFLCTWAVYKYSGEFREIGTVIQ IAETLWEQVLKPLGDLNMEENIROSVTNSIKAGLTDVSHHARL KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFAKTCVDPWLLERHTCPMC KCDILKALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET ASSGYASVQGTYEPPLLEHVQSTNESLQLVNHEANSVAVDViPH VDNPTFEEDTPNQETAVREIKS
6854	1148	585	HESYIGTFDPGEELCVCAA10WLQDNNSASYFLNRLKVYEFSTQAK PVKNTPLRMWIYSHHIYQODLRKKI1DVGKRLDVTGFCMTGKPG IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR LFHSFELLLEAHGDYGLRNDYHMMNLGQFLEFLKKHKSEHVFQI LFGIESKSSDS
6855	1913	1148	GRVGGRVGRICSPSLSGANEYIASTDTLKTTEVLLFTDQFDDLAK EEPTSLFQDSETKGESGLVLEGDKIEHQ1FEDLDKKLALASRF YIPEGCIQRHAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI QLTYSRWSVEVEDSCSDAIERMYCAPEVGAIETEACDWWSL GAVLFELLTGKTLVECHPAGINTHTLNMPEWVSEEARSLIQQL LQFNPLERLCAVAGVAGVEDIKSHPFFTPVWDWALMR
6856	1617	997	VTOLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQOR TVYRLTLVKAUNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA SSLTMHVPWHEEEVVQFVRELVDLIPYEYIACEHEHSKCLLIAH RKFKIGWEWTWINYNRFOELIQEYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPKDTRHQRKNKSKA1SGC
6857	1	617	KGPFEATAMVCVCSERNCRONHIKEPSHSAAQWCGSPTLSAPNH KLMAMEEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQORLSDEDGTNMLHQLVRQEMAVCPQLSEFLDSLRLQYLRGT TGVRNCFHITAVRLSDGF2FVIVYEFWETEEAWKRHLQSPFLCKAF RHVKVDTLSQLPEALSRILVPAAWCTVGRD
6858	2	669	RSRGIKDFENDPPLSSCG1FQSR1AGDALLDSGIRISSVFASPA LRCVOTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPILLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEKWELVNPPVKTLLHGANAAPNWRNWI GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDDSGGYNLSDIQSPSSTGLLKSG KTNMVESLPELLTSDEGSYAGVGSPRDLQSPDFTTGFBHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPVVDLRTIMEIESRQKCGATPKSHLGKT VSHGVKLSQKRMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEKKSVTSHSSGDHVKKVSKFGIEN SQAPKIVRCSTHGTPGPEGNHISDLPPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQOEALIIRSREKPLALIQIEHAIQDLLVF YEAFGNPEEFV1VERTPOGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKKRGIFFPKVATN1MRAWLFQH1LTHPYPSSEQKKQLAQ DTGLTI1QVNNWFINARI1IVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNGMDGQWHYM
6861	1889	1515	DKDKKRQKKRGIFFPKVATN1MRAWLFQH1LTHPYPSSEQKKQLAQ DTGLTI1QVNNWFINARI1IVQPMIDQSNRAVSQGAAYSPEGQP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MGSFVLGQQHMGIRPAGPMSGMGNMGMGDGQWHYM
6862	2	471	EEIDREFHNKLKLKEDKLEKOEKPVNGEDKGDSGVDTONSEGNA DEEDPLGPNCYYDKTKSFFDNISCDNRERRPTWAEERRLNAET FGIPLRPNRGRGGYRGRRGLGFRGGRGRGGGRGGTAPRGFRG GFRGGRCREFADFEYRKTIAFGP
6863	2216	481	PQEPAKSEFSQVANSNTIPLFLPQPNCTKDNPGCKQVCSTVGG AICSCCPGAIMADGVSCECDCECLMGAEDCSRRQFCVNTLGSF YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL GSFHCHYKALTCEPGYALKDGECEDVDECAMGHTCQPGFLCQNT KGSFYCQARQRCMDGFQDPEGNVCVDINECTSLSEPCRPGFSCI NTVGSYTCORNPLICARGYHSADDGTKCVDVNECETGVHRCGEG QVCHNLPGSYRCDCKAGFORDAFGRGCIDVNECWASPGRLCQHT CENTLGSYRCSCASGFLLAAGDKRCEDVNECEAQRCSECANIY GSYQCVCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS YOCACPQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS FRCLRFECPPNYYQVSKTKCERTCHDFLEQNSPARITHYOLN FQTGLLVLFAHIFRICPAPAFGTDTIALNIKGNEEGYFGTRRLN AYTGVVYLQRAVLEPRKDFALDVEMLWRQGSVTTFLAKMHIFFT TFAL
6864	2	2933	LADSSPSNLQIIKELLSMHQDPALTKEDFYLPVDSRSSSG FVGLRNGGATCYMNAAVFOOLYMQPGLPESLLSVDDDTDNPPDSV FYQVQSLFCHLMESKLQYYVPEFWKIFKMMNKELYVREQQDAY EFFTSQSLIDQMDEYLKMKGRDQIFKNTFQGIYSDQKICKDCPHRY EREAFMALNLNGVTCSLEISLQDFVRGEVLEGNSNAYCEKCK EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRS1KYDEQIRFP WMLNMEPYTSGMARQDSSSEVGENGRSVDQGGGSPRKVALT ENYELVGVIVHSGQAHAGHYSFIKDRRGCGKGKWFNDTVIE EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAIMLFY QRVSDQNSPVLPKKSRSVVRQEAEDLSLAPSPEISPQSSPR PHRPNNDRSILTKLVKGEXKGLFVEKMPARIYQMRDENLKF MKNRDVYSSDYFSFVLSLASLNATKLKHPPYPCMAKVSLOLAIQ FLFQTYLRTKKKLRRVDEEWIATIEALLSKSFACQWLVEYFIS SEGRELKIFLLECNRVREVRAVATILEKTLDSALFYQDKLKS HOLLEVLLALLDKDVPENCKNCAQYFFLFTVQKQGIRAGDIL LRHSALRM1SFLLGASRQNQIRRSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKORPPIISIAPSSPLPLHEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYCCFCNEHFSFTMLH FIKNQLETTAPPHELQNTFQLLHEILV1EDP1QVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTQLONSVNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVTTPVQVRLQSPQSQGSMPSCNRS CSCSRGSPVEDGKWHYGRSYLHLFYEGYAVPPKLEGIGEgefLV LDQRAADYDQNALGTCRLAGTALCVAAGVLLAICLFWAMIGWLQ DTKAEPFLPDEADSHVEVFGDEPEQQLSP1FERNASCGSWFSPPAS PFGQSSVQTQPKRDS
6866	1571	491	DCPRPRVITYGLRATCMRDLWDWAWINAVSAFKALEQDLPVNIF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFVMVEVKCRDQDFHSGTFFGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAYEKFQVTRHLEDVFSKRNSNNKMMVSMIL GLHPWIANIDDTQYLAKRAIRTVFGTEPDMDIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL EMAQLH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6867	2833	1704	GTRIMSPQPKQKELAGFVRQXMLLDYSVYMGRCVPQESRSPORSP <sup>1</sup> LQSAESSPTAGKKLPEVPPSEEEEQEAWNALLGRIFWDFLGEK <sup>2</sup> YWSDLVSKKIQMKISKJKLPIFYMFNELTLETDMGVAVPKILQAF <sup>3</sup> KPYVDHQGLWIDLEMYSNGSFLMTLETKMNLTKLGKEPLVEALK <sup>4</sup> VGEIGKEGCRPRAFLADSDEESSAAGSSEEDDAPEPSGGDKQL <sup>5</sup> LPGAGYVGGHRTSKIMRFVDKITKSKYFQKATEFEFIKKKIEE <sup>6</sup> VSNTPLLLTVEVQECRGTAVNIPPPPTDRVWYGRKPPHVELK <sup>7</sup> ARPKLGGEREVTLVHTDWEKLEQEFOKVVFVMPMDDVYITIM <sup>8</sup> HSAMDPRSTSCLLKDPVVEAADQP <sup>9</sup>
6868	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD <sup>1</sup> KATFESOMSVMRGQIINLNLTQALRDKSPFQLVQ1PCVIVERSQG <sup>2</sup> GSQGRIVHLNSNFTQTVNCRKPPFSSW <sup>3</sup>
6869	3	1615	MYMERMDPKTFWESVEHLKANKNEIPQLVGEIYQNFVYES <sup>1</sup> KEISVEKSLYKEIQCQLVGNKGIEVFYKIQEDVYETLKDYYPS <sup>2</sup> FIVSDLYEKLLIKEEKHASQOMISNKDEMGPRDEAGEEEAVDDGT <sup>3</sup> NOINEQASFAVNKLRELNEKLEYKRALNSIQNAPKPDKKIVSK <sup>4</sup> LKDEIILIEKERTDLOLHMARTDWWCENLGMWKAITSGEVTEE <sup>5</sup> NGEQLPCYFVMVSLQEYVGGVETKNWTPKRLSEFHNLHRKLSEC <sup>6</sup> VPSLKKDOLPSLSKLPFKSIDIHTFMEXFENQLNKFLQNLLSDER <sup>7</sup> LCQSEALYAFPLSPSFDFYLKVIDVQGKNSFSLSSFLERLPRDFF <sup>8</sup> SHQEEETEEDSDLSDYGDDVDGRKDALAEPFCMILIGEIFELRGM <sup>9</sup> FKWVRTLIALVQVTFGRTINKQIIRDTVSWIFSEOMLVYYINIF <sup>10</sup> RDAFWPNGLAPPTTIRSKESOQETKQRAQQKLLENIPDMLOSL <sup>11</sup> VGQQNARHGIKIFNQETRANKHLLYALMELLIELCPELRV <sup>12</sup> HLDQLKAGQV <sup>13</sup>
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPOPPNILLMLDDMGWG <sup>1</sup> DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT <sup>2</sup> GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLPPELLKKAG <sup>3</sup> YVSKIVGKWHLGHRPQFPLKHGFDWEFGSPNCHFGPYDNKARP <sup>4</sup> NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLCALDFIKRQ <sup>5</sup> ARHHPPFLYWAVIDATHAPVYASKPFLGTSQRGRYGRDVAIREIDDS <sup>6</sup> IGKILELQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC <sup>7</sup> GKQTTFEGGMREPALAWWPGHVTAGQVSHOLGSIMDLFTTSLAL <sup>8</sup> AGLTPPDRADGLNLPTLLQGRLMDRPIFYYRGDTLMAATLG <sup>9</sup> QKAHFTWTNSWENFROGIDFCPGQNVSGVITHNLEDHTKLPL <sup>10</sup> IFHLGRDPGERFPLSFASAEYQEALSRTSVVQOQHEALVPAQP <sup>11</sup> QLNVCNWAVMNWAPPGECEKLGKCLTPPESIPKKCLWSH <sup>12</sup>
6871	209	1126	RMSLNPF1FLKRSEENSSKFVETKQSQTTSIASEDPLQNLCLAS <sup>1</sup> QEVLQKAOQSGRSKCLCGGSRMFYCYTCYVPVENVPIEQIPLV <sup>2</sup> KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNITYTPCIEYE <sup>3</sup> EKDHEVALIFPGPOSISIKDISFHQLKRIQNNVRGKNDPDKPS <sup>4</sup> FKRKRTREEQEFCDLNDSKCKGTTLKKIIIFIDSTWNQTNKIFTDE <sup>5</sup> RLQGLLQVELKTRKTCFWRHQKGKPDFTLSTIEAIYYFLVDYHT <sup>6</sup> DILKEKYRGQYDNLFFYSFMYOLIKNAKCSGDKEKGKLT <sup>7</sup>
6872	880	459	FGLMMVVLSSLIFMKGNCVRREDLIFNLFKLGLDVRETNGLFGNT <sup>1</sup> KKLITEVFVRQKYLEYRRIPYTEPAEYEFWLWGPRAFLETSKMLV <sup>2</sup> LRFFLAKLHKKDPQSWPFLHYLEALAECEWEDETDDEDPDTGDSAHG <sup>3</sup> PTSRPPPR <sup>4</sup>
6873	1929	955	DEQAVLCSKDKTYDLKIADETSNMLLFIGCKTPDQLKKEDSHCN <sup>1</sup> IIHTEIFGFSNNYWELRRRPLKKLKKLMLMENYEGPDSQEK <sup>2</sup> DSNSSKYTTEDLLDQIQASEEEEIMTQIQLQVNACKIGGYWILEF <sup>3</sup> DYEMKLLNHTQLVDSSESWSFGKVPLNTCLQELGPLEPEEMIEH <sup>4</sup> CLKCYGKKYVDEGEVYFELDADKICRAARMLLQNAVKFNLAEF <sup>5</sup> QEVAWQOSVPEGMVTSLDQLKGALVDRHSRPEIIFLLKVDDLPE <sup>6</sup> DNQERPNSLFSLREKWTTEEDIAPYIQDLCGEKQTIGALLTKYSH <sup>7</sup> SSMQNGVKVYNSRRPIS <sup>8</sup>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6874	1	307	DEIADHVNNSAAVNVEEGTKNLGAAKYKLAALPVAGALIGGMVG GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIIQRKCKKMMEKLTS SCIIDLPSQTDKKCS
6875	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFIIHSISLLNAEEHSTIA TLLRIKEEKEEDLMKGSGFVSVLEWVTTISKKNODKKYEIIKRDI LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI SEKTEPELWYQOQTEDDLTIRLPEDNTKED1Q1QFLPDHINI VULKDHOFLLEGKLYSSIDHESSTWIIKESNSLEISL1KKNEGLTW PELVIGDKQGELIRDSAQCAAIAERLMLTSEELNPNPDPKEKPP CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVLGSNQYLFSSV IVDPKEMPCFCLRHDVDAALLWQPHSSKQDDMWHEIATFNLGYV QASKRDKKFFACAPNYSAALECECLRRVFIYRQPAAPMSTVLYNR KEGRQVGQVAKQQVASLETNDPILGFQATNERLFLVTTKNLFLI KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTTSRTSVTKLS LHJKPRMPPCDFMPERYQVIFLVNSGEANELAMLMARAHSNNI DIISFRGAYHGCSPYTLGLTNVGIYKMEPLPGGTGCOPTMCPDVF RGPGWGGSHCRDSPVQTIKCKSCAPDCCQAKDQYIEQFKDTLSTS VAKSIAGFFAEPPIQGVNGVVCQYPKGFLKEAFELVRARGGVCIAN EVCTGFGRLGSHFWGFOFHDVLPDIVTMAGKIGNGFPMAAVITT PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIEENLQENSQ EVGTYMLLKFAKLRLDEFIIVGDVRGKGLMIGIEMQDKISCRPL PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIASPMCITKPEVDF AVEVFRSALTQHMERRAK
6877	1	776	GTSFSPARAYAPPTERKRFYQNVSIQEGGFEINLDEHRKLKTP QAKLFTVPUSEALAIAVATEWDSQQDTIKYTMHLLTLCNTSLDN PTJORNKDQLIRAAVKFLDTDTICRYVEEPETLVEIQRNEWDPII EWAEKRYGVEISSTSIMGPSIAPKTRVLVSHIASNTWALOG IEFVAAQLKSMVLTGLLIDLRLTVEAQVLLSRLEEEYCIQKGWN IEWADHYELQELRARTAAGTLFIHLCSSETTVKHLKLKE
6878	933	263	QTLOGDFKNAEMIDFNIRIKNVTRSDAGKYRCEVSAFSEQQN LEEDTVTLEVILVAPAVPSCEVPSSAALSGTVVELRCODKEGNPAP EYTWFKDGIIRLENPLRGQSOTNSSYTMNTKTGTLCFTNTVSKLD TGEVSCEARNSVGYRRCPGKRMQVDDLNISGIIAVVVVVALVIS VCGLGVCYAQRKGYSKETSFQKSNSSSKATTMSENDFKHTKSF II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDEVLRVALPDGTTVTVRK KNSTTDOVYQAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE FPHLYIYONTSAVPGTCLTIRKWLFTTEBEEILLNNNDCLAVTYF FHCAVDDVKKGYIKAEEKSYQLQKLYEQRKVMVYLNMLRTCEGY NEIJFPIACDSRKGHVITASITHFKLHACTEEGOLENQVIA FEWDEMQRWDTDEEGMAMCFEYARGEKKPRWVKIFTPYPNMHE CFERVFCELKWRKEEY
6880	2110	1437	RKDNCATAKEWTFPEAKWNNTARVFSHIRLGGMGHVLLIVOCFISS MANJYNEKILKEGNLESIFIQNSKLYFFGILFNGLTLGLQRS NRDGKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMPH VILMAQVITVIITTVSVLVLDFRPSLEFFLEAPSVLISIYNAS KPCVPEYAPRQEIRDLGSGNLWERSSGDGEELERLTKPKSDESD EDT
6881	263E	2244	NDSKWEDEJHVITGALKMFFRELPEPLIFTFNHFNDPVNAIKQEPR QRVLAVKDLIRQLPKPNQDTMQLFRHLLRRVIENGKRNRTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNZQIVELLLELSSIFGR
6882	1	850	GIPFAQLWIYPVKSCCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNMVTARQEFRLVLIISLTCDDGDTLTLSAAYTKDLLLPIKPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH MRPHFPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KVKATNFRPNIVISGCDVYAEDESWDELLIGDVELKRVMACSRCI LTTPDPDTPGVMRSRKEPLETLKSYRQCDPSERKLYGKSPPLFGQYF VLENPGT1KVGDPVYLGC
6883	2794	2256	NEKLKLNONLKLFLITLTYCVLSLHGWGPGIHLQKEGAFPVQTQR ALCOLLYDLRVLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI DPPFDLDPVTPHLSNSLNHLRLVORTSVLFLGLVTGTENQLAPRSSTF NSQEPHNILPLASSQIRFGLLPLSMTSTRYAKSTRNIEFTKAQYD ANC
6884	?	99	EPEERVTAEEAVKPRETSEPRAAAQRFCKEFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVAESXKGNASNPQPGFQDV LCDSPYQQLISAFDFIKNQSGQEASFMIWTGDSPPHPVVPVPELSTD TVINVITNMTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV YNAVANLWKPWLDEEA1STLRKGGFYQSQKVTTNPNLRIISLNTN LYYGPNNITLNKTDPANQFEWLESTLNNSOONKEKVV1IAHVPV GYLPSSONJITAMREYYNEKLIDIFQYSDVIAQOFYGHTRDSI MVLSDKKGSVNSLFVAPAVTPVKSLEKCTNNPGIRLFQYDPR DYKLLDMLCYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES LYGLAKQFTJLDQSKQF1KYYNYFFFVSYDSSVTCDKTCKAFQICA IMNLDNISYADCLKOLY1KHNY
6886	?	1341	OCGGIPCREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK QARVSQELKKAAKRTVSISEGPDTLGDGMRRERRETLLAPEPEP LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDPKKRRGHSI GGAPEORYC1IPVCVAARLPTRAQDVLD AHLSEVNARFQGPNSS LLATGGADRL1IHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY CVLAATYNOAAQLWKVGEAQSKETLSGHKDVKTAAKFKLTRHQA VIGSRDRTVKEWDLGRAYCSRTINVLSYCNDDVVCGDHIIISGHN DOKIRFWDSRGPHCTQV1PVGRTVTSLSHDLQHLHLLSCRDNT LKVIDLRVENIQRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD GALYIWVDTGKLESRLQGPHCAAVNAVACYSGSHMVSDQGR KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAOLOGGCCPRGPWCPQHG GQCRRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG TYRSOSPRSPAGFPRGGTGWPEPAVCLCVAVGPORLSSPGLVY NAGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT FASNNVTDMPDLPFTDELKQRYCLDTWGVWPRPDWLLTSFWGG DLRAASNI1FNSGNLDPWAGGGIRRNLSASVIAVT1QGGAHLD LRASHPEDPASVVEARKLEATI1GEWVKAARREQQPALRGGPRL S1.
6888	1	992	FVAYVKKEIPHIVVTHCLLNPHALV1KTLPTXLRDALFTVVRVI NFIKGRAPNMRHLFQAFEE1GIEYSVLLFHTEMRWLRSRGQILTH 1FEMYEEL1NOFLHHKSNL1VDFGENKEFK1H1LAYLADLFKHLNE LSASMQRTGMNTVSAREKLEAFVRKFPPFWOKRIEKRNFNTFPFL EE11VSDNEGIF1AAEITLHLQQLSNFFHGYSIGDLNEASKWI LDPFLFM1DVFVDDSYLMKNDLAEIRASGQ11MFFETMKLEDFWC AOFTAEPNLAKTALE11MPFATTYLCELGFS1TFTFQNKVPEAA L1LSDDDIRVAISKKVPSFLGH
6889	1	1534	L1LENQ1KEEREQDNSESPNGRTSP1LVSONNEQGSTLRLD1TTT AGKLRVCGSTDAGIAFAPVYSMGAPSSKSGRTMPN1LDD1IASV ENK1PPSKTSK1NVKPELKEEPEES11SAVDENNKLYSDIPH1SW 1CEKH1LWLKDYKNSSNWLKFKECWVKOCOPAVVSGVHKKM1SL WKAES1SLDFGDHQADL1NCKDS11ISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSSGEDFKTMMMPARYEDLLKSLPLPEYCNP EGKFN1ASHLPGFFVVRPDLCPRLCSAYGVVA1KDH1GTTNLH1 EVSDVNVN1LVYV1GNG1LSKAG1LKKPEEEDLDD1L1RKR1LK DSSE1PGALKWH1AGKD1V1DK1REFLQK1S1KEQGL1EVLP1AG1LHQV1C

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NFHSC1QVTEDFVSPHELVESFHLLTKEEINYDDKLQVK N1LYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLERALVHHXATAETCNSPPCGAKDSLIFGAITCF TGFLGVDTGAGATRWCRLKTQRADPLVCAGMIGSAIFICLIFV AAKSSSIIVGAYCIFVGETLIFGSNWAITADILMYVVIPTRRATAV ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA LMLCPFVVVLGGMFFLATLFFVSDRARABQVNQLAMPPASVK V
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ LLLKTKVLYNNMEDNNPEVROAAAYGLGVMQAQFGGDDYRSLCSE AVPLLVKVIKRAHSKTKKNVIACTCISAJGKILKFKPNCVNVD EVLPHWLSWLPLHEDKEEAQTLSFLCDLIESNHPPV1GPNNSD LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC VSQLDDEQQEALQELLNFA
6892	3	876	RSVAASGPAGAWGTDHYCLELLRKRDYEGYLCSSLPAESRSSV FALRAFNVELAOKVDSVEKT1GLMRM0FWKKTVEIDYCDNPPH OPVAIELWKAVKRHNLTKRWLKMKVDEREKVNLLDKAYRNKELE NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCRLA TPYHGSSRRKVFPLPMDICM1LHGVSQEDFLRRNQDKXNVRDVYDIA SOAHLHLKHARSFHKTIVPKAFFPLQTVSLEDFLKKIQRVDFD IFHPSLQKNTLPLPLYI1QSWRKY
6893	1	842	DGERKMSMVERTFSEINAKEEQYSLCQELCSELAQDLOKERLKG RTVT1KLNVNFEVKTRASTVSSVNSTABEI1FAIAKELLKTEID ADFPHPRLRLMGVRISFPNEEDRKHQQRSSI1GFLOAGNQALS ATECTLEKTDKDKFVKPLEMSSHKSSFFDKKRSERKWSHQDTFKC EAVNKQSFQTSQPFQVLUKKKMNENLEI1SENSDDCQ1LTCPVCFR AOGCISLEALNKHVDCLDGP5ISENFKMFSCSHVSATKVNKE NVPASSLCEKQDYEAH
6894	1742	1463	TT1CKPLVPREHQFYETLPAEMRKFTPOYKGKSQ1LEGPLPHWRG DVRDRGHGRPWQPSLEPSLPPTLCPFSLSSFSSWPSAQHLPSP VFNFW
6895	2379	478	VTYVELCOLASPTALLIMRTVLDLIVEDLQSTSEDEKQQYTSQT TRLLALLYALASHKACKLAI1HLHLLNGT1KGDERYAE1FQDILLAL VRSPGDSVIRQQCVEVVTTS1L0SLCDODIALILPSSSEGS1SEL EQLSNSLPNKELMTS1CDCL1LATLANSSESSYNCL1TCVRMMFL AEHDYGLFLHKSSLRKNSALHSLLKRVVSTFSKDTGECLASSFL EFMRQILNSDT1GCCCCDNGLMVEVEGAHTSRM5INAELKQLL QSKEESPENLFLLEKLVLEHSKDDDNLDSSLDSVVGKQML5 SGDPLPLSDQDVEPVL5APESLQNLNFNNRTAYV1ADVMDDQLK5 MWFTPPQAE1IDT1DLDLVKVDLIELSEKCCSDFDLHSELERSFL SEPSSPGRKT1TKGF1KGKHHKETFITSSGKSEYIEPAKRAHV PPPRGRGRGFGQG1FPHD1FRQKONTSRPPSMVDDFVAAES KEVVPQDG1PPPKRPLKVSQK1SSRGFGSGNRGGRAFH5QNR FTPPASKGNYSRRECTGRSSWSAONTPRGNYNESRGQQSNFNRG PLPPLRPLSSTGYRPSPRDRASRGRRGGLCP5WASANGSGGSRG KFVSGGGSGRRHVR5FTR
6896	1	555	GNIV1OKKKYNNKQH11PENVT1DS1KDEGDLRNGWL1KTPTKS FAVYAAATATEKSEWMNHINKCVTDL1SKSGKTPSNEHAAVVVPD SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFL1PSQ SSKPVR1CDPCYDLSAGDMATCQPAR5DSY5QSLKSP1NMDSD DDDDDDSSD
6897	3	920	GDGLMHEVNGLMERPDWETA1OKPLCSLPAGSCN1ALAASLNHY AGYEQVNTEDLLTNCT1LLCRL1SPMNL1L5LHTASGLRLFSVL SLAWGFIADVDESEK1YRRLGEMRFTLCTFL1LAALRTYRGR1A YLPVGRVGSKTPASPVVQQGPVD AHLVPLEEPVPSHWTVPD DFV1VLALLHSHLGSEMFAAPMGRCAAGVMHLFVVRAGVSAML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LRLFLAMEKGRHMEEYECPYLVVVPVVAFLLEPKDGKGVFAVDGE LMVSEAVQGQVHPNWFWMVSGCVEPPPSWKPOQMPPEEPL
6896	919	346	QKTVTAVASLLKGRQGIYTENERRMGAVIDKIRFFKIMLVLIICW LSNIINESLLFYLEMQTDINGSSLKPVRTAAKTTWFIMGILNPA OGFLLSLAFYGTGCGSLGFOSPRKEIQWESLTTSAECAHPSPL MPHENPASGKVSQVGGQTSDDEALMSLSEGSDASTIEJHTASESC NKNEGDFALPTHGDL
6899	120	827	MKVRKNNDAYLLDKNINMDCFISCCFFKKMLTTLMFHSIGILSL LEHGEETYFSLSPCAYARSILTVPVWELGGKVSNCAKTGYSASI TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS NGETKVVLDLTKLAVTKRVRPLEKQDPFESRRLWKVNVTDSLRES EIDKATEHKHTLEERQTEERHRTETGTWKTKYIFIKEGDGWVY HKPLWKIIPTTQPAAE
6900	3	451	TEVLGSIGIHELRSSSTSALHHALEESASLLTMFWRAALPSTHIP VLPGKVGESTERELLELRTKVSOQEQLLOSTTEHLKNANQQKES MEOFIVSOLTRTRHDVLLKARTNLEVRKLLHQSEAPSLSPTHHHPP LADLVGDSWPALRFOEK
6901	1	203	DDNMVQRLETDFKMTLQQQSTLEQWAALWDNVMMQALKPYEGRP SFPKAAROFLLKWSFYRYHLGFS
6902	2	267	GAPPPPPSOPPRQPOAAPSSEPHSDLTNFNFSALEQAGAOGA SDMPEPEPSLDLLPELTNPDELLSYLDDPPDLPNSNDDLLSFENN
6903	1	149	RINQVYRQGPTGIHILVIDQMVQNFDQDESCFLFSTVKAESSDG IHIILK
6904	464	2092	MEASLPSLSCVLACGDVEGKFDILFNRVOAIQKKGNSNPDL VGNFFGSGTODAEEWVKTG1KAPIQTYVLGANQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGY SPKDVSLLRMMLCCTSQQPKGVDDILLTSPWPVCVGNFGNSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYERLPYRNHHILOEN AQHATRFIALANVGNEPKKKYLYAFSIVPMKLMDAAEVLVKQPPD VTENPYRKSGQEAS1GKQILAFVEEACOFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGCPWCFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILP1GHYQSVVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHLQLQVIPVPIASCSTDDIKDAF ITQAQEQQIELLEIPEHSDIKCIAQPGAAFYVELDTGEKLFHR IKKNFPLQFGREVLASEA1LNVPDKSDWRQCQISKEDETLARR FRKDPEPYDFTLDD
6905	1	226	VSKTGEAETITSYHLYFALGVYFTLYLFNWIWRYHFFEGFDLIA VAGLVQTVLYCDFFYLYITKVLKGKQLSLPA
6906	3	611	SYDDHNCIHIDFITAASNLRAKMSIEPADRFTKTRIAGKII ATTATVSGVALEMVKTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIIRNGISFTIWDRTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPMPPGHAKRLKLTMHKLVKPTTEKKYVDLT SFAPDIDGDEDLPGPPVRYFSDHTD
6907	2	2228	LRGVPVWAAGAFRFSSEESTSHLIMSRFSQRLTRYSGDDDG SSSGGSSVAGSQSTLFKDSPLRTLKRKSNNMKRSLPAPQLGPSS DAHTSYSESLVHESWFPPRSSLLEELHGDANWGEDLVRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSSEDDYVGYSDVDQOSS SSRLRSAVSRAGSLLWMVATS PGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTERRFSSLKTFWLFLPLLLLCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRADECWEARDSSPHFQAEQRVMSRVHSL ERRLEAIAEFSSNWQKEAMRLERLRLQAGPGOGGGGGGLSHED TLALLEGLVSRREAALKEDFRTAARIQEEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTOESFQESSVKELRRL DOLAGLQOELAALALKQSSVAEEVGLLPQOIQAVRVDVESQFPA WISQFLARGGGGRVGLLQREEMOQLRELESKILTHVAEMQGKS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AREAAASLSLTQKEGVIGVTEEOVHHIVKQALQRYSEDRIGLA DYALESGGSVISTRCSETYETKTALLSLPGIPLWYHQSPRVI LQPDVHPGNCWAFQGPOGFAVVRSLSARIRPTAVTLEHVPKALSP NSTISSAKDFAIFGFDDEDLQQEGTLLGKFTYDQDGEPIQTFFH QAPTMATYCVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRGLGSRILGLOGCFAARLLYPRFQSRC POGVEDGDKPQPSSKTPRIPK1YTKTGDKGFSSTTGFERRPKDD QVFEAVGTTDELSSAJGFALELVTKEGHFTFAEELQK1QCTLQDV GSALATPCCSAREAHLYYTTFKAGPILELEQWIDKYSQLPPLT AFILPSGCKISSALHFCAVCRRERRVVPVQMGEDANVAKF LNRLSDYDYLFTLARYAAKMEGNQEKIYKKNDPSAESEGL
6909	3	405	GRLLAVGTVTDLYGQRSSAPEQELLVQDATPVNSNLLPEKAFSDIP SPYLRGT1KMMQAVRQAFQDQDDRRRTWDGRPLTMAATFDDCLYA LCVVDTICKRSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS LYC
6910	1	1068	LVPVVV1D5YYGGKLVIAPLNNIVLYN1FTPHGPDLVYGTPEPWYFY LINGFLNFNVAPALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT LAPMYIWFI1FFIQPHKEERFLFVYVPLICLCGAVALSALQHSE LYFQKCYHFVQFRYRLEHYTTSNWLALGTFLFGLLSFSRSVA LFRGYHGFLDLYPEFYR1ATDPT1HTVPEGRPVNVCVGKEWYRF PSSFLPDPWQLOF1PSEFRGQLPKPFAEGLATRIVPTDMNDQ NLEEPSRY1DISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY RPFLDASRSKLLRAFYVPFLSQDQYTYYVNYTILKPRKAKQIRK KSGG
6911	1184	966	GEDAEEMETGNVANLIS1FGSSFSGLLRKSPGGGREGEEGEESG PEAAEPGQJCCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSF0MLFT1STGSAKQSYEDAYRCIKSS1LGS1 SGGTDI1ISCFMGNFSLPVYKGE1QARNLGMAVEAWNEEGKAW GESGEGLVCTKPIPCQPTFWNDENGNKYRKAYFSKFCPIWAHD YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE DSLCPQV1KYREERV1FLFLKMASGHAFQDPLVKRIRDADMGL SAHHVPSL1LETKG1PYTNGKKVVEAVKQ1IAGKAVEQGGAFS NPETLDLVKD1PELQCF
6913	1643	1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKS1AGYPGTLI1PYRCDSLNEEDILSMFSAIRSOHSGVDI CINNAGLARPDTLLSGSTSGWKDMFNVNLALS1CTREAYQSMK ERNVDDGHJ1IN1NSMSGRVPLSVTHFYSATKAV1ALTEGLR QELREAQTH1RATC1PGVVE1TQFAFKLHDKDPEKAATYEQMK CLKPEDV1EAVIYV1LSTPAH1Q1GDI1QMRPTEQVT
6915	254	652	GRSLSFKTF1I1WV1L1S1Y1O1G1G1L1M1Y1G1A1V1F1E1S1F1T A1L1L1TE1L1M1V1A1T1V1R1T1W1H1W1L1M1V1A1E1F1L1G1C1D1F1R1 V1A1F1T1T1V1F1L1W1K1V1S1A1T1V1V1S1C1L1P1Y1V1L1K1R1R1K1L1S1P1S1Y1C1K1L1S1
6916	254	652	GRSLSFKTF1I1WV1L1S1Y1O1G1G1L1M1Y1G1A1V1F1E1S1F1T A1L1L1TE1L1M1V1A1T1V1R1T1W1H1W1L1M1V1A1E1F1L1G1C1D1F1R1 V1A1F1T1T1V1F1L1W1K1V1S1A1T1V1V1S1C1L1P1Y1V1L1K1R1R1K1L1S1P1S1Y1C1K1L1S1
6917	254	652	GRSLSFKTF1I1WV1L1S1Y1O1G1G1L1M1Y1G1A1V1F1E1S1F1T A1L1L1TE1L1M1V1A1T1V1R1T1W1H1W1L1M1V1A1E1F1L1G1C1D1F1R1 V1A1F1T1T1V1F1L1W1K1V1S1A1T1V1V1S1C1L1P1Y1V1L1K1R1R1K1L1S1P1S1Y1C1K1L1S1
6918	28	921	PEAGTRSWREPDPEDLRRFLLSACRSFP0WLPGGGGQVSSCS DTDV1Y1L1L1V1K1S1E1P1G1F1A1R1Q1V1R1E1T1W1G1S1P1 V1G1E1A1G1P1D1L1S1L1V1A1E1S1R1Y1S1D1L1W1D1F1L1V1P1F1N1Q1T1L1K1D1L1L1L1A1W1 L1G1R1C1P1T1V1F1V1L1R1Q1D1A1F1V1H1T1P1A1L1H1R1A1L1P1A1S1R1S1Y1L1G1E1 V1F1T1Q1A1M1P1R1K1P1G1F1Y1V1P1E1S1F1E1G1G1Y1P1A1S1G1G1Y1V1A1G1R1L1P1 L1L1R1A1A1R1V1P1F1P1F1E1D1V1Y1T1G1C1R1A1L1G1L1V1P1Q1A1H1P1G1F1L1T1A1R1 ADHCAF1R1N1L1L1V1R1P1G1P1Q1A1S1R1L1W1K1Q1D1P1R1Q1C1



SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
			DGYPLPTFDTSPLDGVDPDPAFFAAPPMPGDCPAAGTYSYAQVSDYAGPPEPPFAAGPMHPRLGPEPAGPSIPGLLAPPSSALHVVY GAMGS PGAGGGRGFOMQPOHOHQHOHQHPPGPGQQPTPPPFEALPCR DGT DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNL PD SHCAASSVSDASSAVVYCNYPDV
6927	2	1484	LTLCGDIDCLMLAONANRRAAHLLEEHYQTKEOELIHLSLHRESS CGFAWATDLSLTDLESQLSVSKCYEAEANEIILQFRDLKSQNPEH YVQVLKRMCNIRNEIGVFYMNQAAALQSERLVSKSVAEEQQQLW KKSFSFCFEKGJHNFESIEDATNAALLCNTGRLMRCIAQAHCGA GDEIJKREFSPEEGLYVNKAIDYYKLALRSILGTRDIHFAVWDSVN WELSTTYFTMATLQODYAPLRSKAAQEIQIEKEVSEAMMKS LKYCD VDSVSARQFLCQYRAATIHLRASMYHSCLRNQVGDEHLRKQH VLADLHYSKAAKLFLQLKDALCELLRVOLERVAFAEQMTS QNS NVGKLKTLGALDIMPRTHEAFQLIQKELIEEFQGPKSGDAAA ADASPSLNREEVVMKULSIFESRLSFLLOSIKLLSSTKKKT SNN IEDDTILKTNKHIYSQQLRATANKTATLLERINVIVI:LLGQLA A GSAASSNAVQ
6928	1086	777	EATIDLINNLLOVKMRKRYSVDKTLSHPWLDQYQTWLDLRELECK IGERYIHTESDDL RWEKYACEQGLQYPTHLINPSASHEDTPETE ETEMKALGERVSIL
6929	1749	607	RDORGYRDEERSPAREPGDVSARTRSGGGGRSATTAMPPPVPNG NLHQHDPDQDLRHNNGNVVAGRPSCSRGP RR A1QK P QPAGGRRSC RCPAAGGLC1QPPDQGT CVPPEPPVPPMDWEALEKHLAGLQFRE QEVRNQGQARTNSTSAOKNERESIRQKLALGSFFDDGPGIYTSC SKSGKPSLSRRLQSGMNLQ1CFVN DSGSDKDSADDSKTETSLD TPLSPM SKOSSSYSSDRDTTEESESILDDMDFLTRQKLQAEAKM ALAMAKPMAKM QVEVEKQNRKSPVADLLPHMPHISECLMKRSL KPTDLRDM7IGQLQVIVNDLHSQIESLNEELVQLLIJRDELHTE QDAMLVDIECLTRHAESQQQKHMAEKMPAK
6930	131	545	FKDTANVFVSLFO/RN NFRHYFIEPSQLKL FYDVTWIVTQV AIV SYT VVPUFVLLSIKPSLTFYSSWYYCILHILGILV LLLL PVKKTQR RKNTHENIQLS QSKFDEGENSLQNSFSTTNNVCNQNEIASR HSSLKQ
6931	2	659	PVERLPNRPACCLL VASGAAEGVSAQSFLHCFTMASTAFNLQVAT PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL LIPSCPGALTD LASSGLARI LQHFS ESKP1CAGVGHVAALCC ATNEDRSWVFD SYSLTGP SVCELVRA PFGFARLFLVVEDFVKDSC ACFSASEPAVHVVLDRHLVITGQNA S T VPAVQNLFLCGSRK
6932	2	1131	FVDSPGQGEQAE EEE EGGI QMNSRMR AHS PAEGASV ESSPGPKK SDMCEGCRSLAAG EPGYI SHDKET SIKYVSHQHPSH P OLF SIVR QACVRSLSCEVCPGREGP I FFGD E QHGFVFSHTFFIKDSLARGF Q RWY SII T JMDR IYLINSWPFLLGKVRGI IDELQGK LKV FEA EQFGC P QRAORMNTAFTPF LHQ RGNNA RSLTS L TS D DNLWACL HTSF A WLLKQ:CGSRLT EKLL EGA PTEDT L VOMEK LAD LEE ESES WDNSE A EEE E KAPV L PEST GREL T QGP A E S S S LSGCG SWQPRK LPVFKSLRHM RQV C G R G T A H H E L R R R A N H G L C L P T R L A S G P S T L KTLQEVTDLSLLGGWLM A QGVGGII
6933	1431	890	SLNLHCTLFFPHQYPA GYPSDKE GKKPKGOSIGQPSCTT KRP I S D D D C P S A S K V Y K A S D S A E I A E A F Q L I T P Q Q Q H L I R E D C Q N Q K L W D E V L S H L I V E G P N F L K K L E Q S F M C V C C Q E L V Y Q P V T T E C F H N V C K D C L O R S F K A O V F S C P A C R H D L G Q N Y I M I P N E I L O T L L D L F F P G Y SKGR
6934	3030	2586	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLA FIV CWTPFFFVQMW SVW D A N A P K E A S A F I I V M L L A S L N S C N P W I Y M LFTGHLFHEL VQRF L C C S A S Y L K G R R L G E T S A S K K S N S S F V L S H R S S S Q R S C S Q P S T A

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTCLNSVERYSPKAGAWESVAPMNIIRRSTHDLVAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKGVAASCMFTRSSS VGAVAVLNNPPPPSTLVSSTSL
6936	1347	567	FSHRROFLSALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLLTCLHFLRKRLQKGEVGLSVETSKPQPVPGGLSRKKVPOEPWATVMEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRAALLQLRLGDPSP LPSPLPNLGPQGPALTPQESENILHTTQDCYNLLACLLQMEPV NYERVREYSQKVLEROPDNAKALYRAGVAFFLQDYDOARHYLL AVNRQPKDANVRYYLQLTQSELSYERKEKQLYLGMC
6937	1	727	AEEFRCCPGRDPPCAFARGWRLDRVYGTFCFCDQACRFTGECFCFDYDRACPARPCFVGWEWSWSSGCADQCKPTTRVRRRSVQQEPONGGA PCPPLERAGCLEYSTPQGQDCGHTYVPAFITSAFNKETRKQATSPHWSHTTEDAGYCMEFKTESLTPHCALENRPLTRWMQVLR YTVCVDCQPPAMNSVLSRCSDGLDSDGNQTLHWAIGNPRCOG TWKKVRRVDQCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDFMQLKRRQSSKEENDSGTLDTVGAVVVDH EGNVAAAASSGGGLALKHPGRVQAAALYCGCWAENTGAHHPYST AVSTSGGGEHLVRTILARECSHALQaedaHQAQALLETMONKFISS PFLASEDGVLLGGIVIILRSRCRCSAEPDSSONKQTLIVEFLWSHTT ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVIAEGGVCRGEP SELTLOACEASQRHFR
6939	3	810	EVTAPRPRQRYSSGHGSDNSSLGELPPAMGRTALFHSSGGSS GYESLRRDSEATGSASSAPDSMSSESAGAASPGARTSLSKSPKRA TGLORRRIIPAPLFDTALGRKPSPLGQWVDSLPPPLAGSLKEPF EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRRLAERKQR LREVOAKKKHLCEELAETOGRMLEPGRWLEQFEDPELEPESA EYLAALERATAALEQCNLCKAHVMVTCFDISVAASAAIPGPQ EVDV
6940	1188	496	CKMAAOPLRHSRSRCATPPRGDFCGGTERAIDQASFITTSMEWDTQ VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFOCAOCHAV LADSVHIAWDLSSLRGAVVFSRVTNNVVLAPFLVGIEGSLKGS TYNLLFCGSCGIPVGFLHYSTHAALALRGHFCCLSSDKMVCYLL KTKAIVNASEMDIQNVPPLSEKIAELEKIVLTHNRLKSILMKLS EVTPDOSKPN
6941	1	713	ELSRADSDPHGPHTCGHVNLNVIIGSNVLALAEAQRAEALGYQA VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFOCAOCHAV LADSVHIAWDLSSLRGAVVFSRVTNNVVLAPFLVGIEGSLKGS TYNLLFCGSCGIPVGFLHYSTHAALALRGHFCCLSSDKMVCYLL KTKAIVNASEMDIQNVPPLSEKIAELEKIVLTHNRLKSILMKLS EVTPDOSKPN
6942	1	246	EDYVERYDPTDTWTMGAPlSMPNTAVGGCLLGDRLYADGGYDG CTYLNTMSEYDPTQTNWTQMASLNIGRAGACVVVIQF
6943	1	739	PMATGDGAKTLAIHVAKTADSIRITWKATLFPASSFRLSWLRLG HSPAGGSITEFLVQGDKTEYLLTALEPKPTYIIICMVTMETTNAY VADETPVCAKAETADSISGPTTTLNQEQNAGPMASLPLAGIIGGA VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKDDYMEESC TKKDONSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK ATHTIGYGTTRGVRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELGTSSERAEQPLSVGRLCSTICNMPKALRT LCVNEFLGWLSPFEGMLLFYTDPMGEVVFQGDPKAPHTSEAYOKY NSGVTMCCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA PGLGTGLATLSRNLYVVLSCITYGILFSTLCTLPSLLCDYYQ SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVIGPLTS VGSANGVMYFSSLVSLVFLGCLYSSLFVIYEIPPSDAADEEHRPL LNV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAOQCGHSPKGPARPVPLKKRGRYDVTRNPFLNKGMAFTLEERLQLGIHGLIIPPCFLSQDVQLLRIMRYYERQCSIDLKYYIILMTLQDRNEKLFYRVLTSDEVKFMPPIVYPTVGLACQHYGLTFRRPRLGLFIIHDKGHLATMLNSWPEDNIKAVVVTDGERIILCLGDLGCYGMGIVPGKLA LYTAGGGVPQQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGKAYDDLLEEFMQAUTDKFGINCLIQFEDFANANAFRLLNKYRNKYCMFNDDI0GTASVAVAGIILAALRITKNKLSNHNFGFQGAGEAAMG\IAHLLVMALE\KEGPVKA\EATRKIW\MVDF\KGLIVQGRDHLNHEKEMFAQD\HPEVNSLEEVVRLVKPTAII1GVAIAAEA\FTEOILRDMASFHERP\IIIFALSNPTSKAECTA\EKCYRVTEGPRGFAS\GSPF*GVLIWEMGKTFPGGRGNNAA*RVPRGWOLGVHSPGDPGHI\DEIFLPDSRAKLPOEVSEOHLSOGRLYP\PLST\IRNVFLRIAIVF\GDYKHNLL\SYYPEPKD\KEAFCKIPGSYTPDYDSFYT\VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPGPGV AHLAPSMASDTFESLMLACTDFCLRNLDTGLYLLDKETLRLHPDIFLPSET\CDRLVNEYVELVNAACNP\EPHE\SFFNPLFRDPRKQPASRRHL\RED\LVQD\QD\LEAIRKQDL\VEL\VLTN\CEKLSAKSLQTLRSFSHSTLGV\PAFFGC\TNILLRKENPGGL\CEDEYLPNPTCQVLVKDFTFEGFSRLRF\LKLGRMIDWVVPVES\LLRPLNSLAALDLSG10TSDAA\FLTQWKDSL\VSLLV\YNMDLSDDIIIR\VVVOLHKLRLHLDISRDRLLSSYYKFKLRTREVLVLFVQKLGNLMSLDISG\HMILENCISISKIGKREAGQTSI\EPSK\SSSI1PFRGFEGGPQF\LGVF\GIFCRLTHI PAYKVSGDKNEEOVLANAEAYTEHRPEITSRAINLLFDIARIERCNQLLRALKLVITALKCHKYDRNQVQVGSAAFLYLTNSEYRSEOSVILRROVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEFOYRRVNELLLSILNPTQDES1QRIAVHLCNALVCQVDNDHKEAVGKMGFVVTMLKLTOKLKDTCQVMFWSW\SAWNITDETNDNCEMFLNFGNGMKLFLDCLNEFPEKQELHNRNMLGLLGNVAEVKELRPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEAWGVCEPOREEVEERMWAAI1QSWDINSRRNIN1YRSEPI1RLLPGISPVSWQHATWALYLNVSVY\PDKYCPLLIKEGGMPLLRIIKMATARQETKEMARKVIEHCSNFKEENMDTSR
6947	2	1682	TSVSTI\PRGLASARPQSRSRWRCCPVWRRSPGRARGRGLKMLNVP SOSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLKSGKDLTG LKGRL1EVTTEELKKHNKKDCWCICIRGFVYNSPYMEYHPGGEDELMRA\GSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLKDYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDLSLVTI\EHIIY\TEGYQFLRNNNS*SSE*FLYSRNY\GLLISYTYW\R*A MRFRK1FLCGL\,CESVGKIEIVLQKENTSWDFLGHPLKHNHSLIPRKDTGLYRYRKCQLISKEDVTHDTRLFCLMLPPSTHQLQVPIQQHVVYKLPITGTEIVKPYTPTVGSLLSEFKEPVLPNPKYIYFLIKIYPTGLFTPEDRLQIGDFVSVSSPPEGNFKISKFQELEDLFLLAAGTGFTPMVKILNYALTD1PSLRKVLMFFNKTDEDI1IWRSQLEKLAPKDRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDKSKVLVC1CGPVFTEQGVRLLHDLNFSKNEIHSFTA
6948	104	58	PDGAHSSFPDEYFTCSLCLSCGVGCKKSMMH\GKEGVPHAKSR CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMCLAKYAWSGYVI1ECPNCGVVYRSRQYWFGNQDPVDTVVRTE1VHVWPGTDGFLKDNNNAQRLLDGMN\MAQSVSELSLGPTKAVTSNLTDQIAPAYWRPNSQILSCNKCATSFKDNDT\KHHCRACGEGFCDCSSKTRPVPERGWGPAPVRCDCNCEYEAR\TRPVSCYRGTSGR\RRRRTQETVE
6949	152	4656	GLRLCLSRP1LTPRGDDSVGGSAMASGAGGVGGGGGGKIRTRRCHQGPIKPYQOGRQOQHQGILSRVTESTVNIVPGWLQRYFNKNEDVC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SCSTDTESEVPRWENKENEDHLYVYADEESSNITDGRITPEPAVSNTEEPSTTTAST\YPDVLTIVSLYRSHLNFSMLESPALHCQPSSTSAPFICSSGFSLVKEIKDSTSQHDDDNISTTSGFSRASDKDITVSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSPSLGNSSLLKTSQLCGSDSPFYPGKTTIYGGAA\AVROSKLRNTPYOA PVRQMQAKQQLSAQSYGVTSSSTARLILQSLEKMSPLADAKRIP SIVSSPLNSPLDRGIDITDFQAKREKVDQSQYPPVQRLMTPKPV SIATNRSEVFKPKSLTPSGEFRKTNORIDKKCSTGYEKNMTPQNREREQESCFSPNFSLPAAANGLSSGVGGGGKMRERHAFVASKP LEEEEMEGPVLPKISLP\ITSSSLPTFNFSPEITTSSPSPINSS OALTNKVMCTSPSSSTGSPMFKFSFIVKSTEANVLPSSIGPTF SVPVAKTAEISSLGSSSTLEPISS\AHVITVNSTCKKTPPEDC EGPFPRPAEILKEGSVLDILKSPGFA\SPKIDSVAQPTATSPVYV TRPAIISFSSSGIGFGESLKGSSWQCDTCLLQNKVTDNKCIAQCQAAKLSRDTAKQTGIEPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCI\QNKPEAIKVACETPKPGTCV\KRALTLTVSESAETMTASSSSCTVTTGTLGFQDFKRFJGSGWECSVCCVSNNNAEDNKC VSCMSEKPGSSVPTSSSTVPSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAK\PGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFK1GVSSDSGYINPMSEGF*FSK\HIVGFKFGVSSSEKPEEVK\QD\KDNFKFGLSFGLSNPVFLPPFQFGVSNLQEEKEELLKSSCAGFRFGTVINSTR VPANTIVTSENKSSFNLGT\ETKSVSVAPLKQCTSEAKKEEMPA TKGGFSGVNVEPASLPSVFLGRTEEKQCEPVSTSLVFGEG KLTMKEP\KC\QPVFSFGEFORQTKIENSSKSTFSMTPKSEKE SEQPAKAT\FAFGAQNTTADQGAAPKDL\SYLNNSSSSSSTPATSAGGG\IFGSSTSSSNPVPATVFGCSENPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSGTAVTPVFGPGASSNNNTTSGFGFG ATTTSSEAGSSSFVFTGPGAPSASPAFGANC\PTFGQSQGASQPNPPGFGS\SSSTALFPTGSQPA\PTGTVSSSSQPPVFGQQPSQSAFGSGTTPNSSSAFQFGS\TTNFNTNNSPSGVFTFGANSSTP AASAOFGSGGGPPFNQSPAFTVGSNGKVNFSSSGTSFSGRKIK TAVRRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSR\RTAE*IMDELHYQDTDS DVPEQRDSKCKVWKTHEEDEOLR\ALR\QFGQQDWKF\ASHFPNR TDQOCQYR\WLRV\LNPD\LVKCPWTKEDQKV\ZLVKKYGTQWTLIAKHLKGRLGKQCRERW\HNLNPEVKKSCWTEEEEDRI\CEAHKV LGNRWAEIAKMLPGRTRDN\VA\KHNWNTIKRKVDTGFLSESKDC KPPVYLLLE\EDKDGLQSAQPTEGOCSLLTNWPSVPPTIKEEEN SEELAATTSKEQEP\GTD\DAV\RTPEPLEEFPKREDQEGSPP ETS\LPYKVV\EAANLIPAVGSSLSEALDL\ESDPDAWCDLSKF DLPEEPAEDS\INNSL\VLQLOASHQQVLP\PRQPSA\LPVSVTEY RLDGHTIS\DLSSRSSRGELI\SPSTEVGGSG\CTPPS\VLK\QRK R\RV\ALPVTEN\TSLS\FLDCNSLTFKSTPV\KTL\PFSPS\QFLNF WNKQD\TLE\LE\PSLTS\TPVCSQKV\VV\TTPLH\RD\K\PLH\Q\KA\AF VTPDQKYSMDNTP\HPTP\KNALE\K\GPL\K\PL\Q\TP\H\LEED\K\ E\VL\SEAGI\ELI\I\EDDIRPE\Q\K\RK\PL\RL\RS\PI\K\VR\K\SL\AL\DIV DEDM\K\LM\MS\TLP\K\SL\SL\PTT\AP\NS\SS\LT\LS\G\I\K\ED\N\SL\N\Q\G\F\ LQAKPEKAAVAQK\PR\SH\FT\T\PA\PM\SS\AW\K\TV\AC\G\TR\D\Q\LF\M\Q\E\ KAROLLGRLKPSHTS\RT\LI\LS
6951	1940	239	AGPDDTMKRS\QALYCQLL\SFLL\I\AL\TEAL\A\FAI\QEPSP\RESL QVLP\SGT\PP\GTM\TAP\HS\STR\HTS\SV\VL\TPN\PDG\PP\PSQ\AA\AP\MA\ TPT\PR\AE\G\H\PP\T\TP\SS\PSL\RQ\PP\I\K\AP\SS\TG\PA\PA\AM\AT\ TSS\K\PE\G\PR\GQ\AA\PT\I\LL\K\PP\G\AT\SR\PT\T\AP\PR\TT\RR\PP\PR\ PG\SS\RK\GAG\N\SS\RP\VP\PA\PG\H\SR\K\EG\Q\RG\RN\PS\ST\PL\Q\K\RP\ LGK\I\FO\I\Y\K\G\N\T\G\SV\EP\ST\LT\PT\PL\W\G\Y\SS\PP\Q\Q\PT\VA\AT\

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TVPSNTSWAPTTSLGPAPDKPGLRRAAQGGGSTFTSQGGTPDA TAASGAVPSP/PSCPAFSAPP*PTGWPQP*LLAYCYPCT SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP THPSRVSESTISGAKETVVA/PS*PTGCPVILSPQWYPQPQAI STAWSPPGPGSLLQQGTSQPMWPRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEEEEEDRQPGEQPEAYGNNTTHPGT TFQQAC\RGAAPEIIPVPLKPLRTQLSEPRSPANGDYRDTGMVP C
6952	658	304	PESEGESEGEMTDRYTIHSQLEHLSQKYIGT\ATPTPPSGSG\CE PTPRLVLLHGPLRSPQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARCELRLCLTTAVRGTSPSVSPVCOSS
6953	1512	349	NWGKTRALASGKHVPPFGKQTNPNKS/VHCD\\$*FRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD PYLELCOCPCLCQLDCGSREQLIAHVYQHTAAVVAKS\Y\CPVC GRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATFNSEKLF EVLNMESLPTVHNEGPSSAEGKDIASFPEVYPAGILLVCNCAA YRKLLAEQTPSVRKWAIRRNEPLEVRORLERERTAKKSRRDN ETPEEREVRMMRDREA\KLRQRMQETDEQRARRLQRDREAMRLKR AIETPEKQRQARLIREREA\KRLKRRLEKMDMMMLRAQFGQDPSAMA ALAAEMNFFQLPVSGVLELDSQLLGKMAFEEQNSSLH
6954	819	1	PPPPFIIPSHPREAGT*AG\KRSGDSECSPFVEQ*A*TRAACQN *PQR*RIVTEGNSPOASAVATPGQGASPAAPRCTP*PSRRHRLP PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR *CAGAAAGRPRRRDRSPRPTPGCCSWSEPRTPPVAWSASAQTPS DAG*AGGR*GQRQRPSTGR*PPGVGAGRSRREGTIPGPNPHPR AS\RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGGAFFNQVGSS VMOAMSTGI
6955	1968	782	PPGRRQVRAQVAGAPVGHGTRARQVKTGRRRAARTMPFLQD WRSPGWSWIKTEDGWKRCECESCQKLERENNHCNISHSIIILNSED GEIFNNEEHEYASKRKKKDHFRNDNTOSFYREKWIYVHKESTK ERHGCTYLGEAFNRNLDSSAIQDIDRFRNYVVKLLQLIAKSQLTS LSGVAQNYFNILDKIVQKVLDHHNPRLIKDLLQDLSSTLCIL /N*RSREVCISGKHQYLDLPIRNYSRLLATTATGSSDD*ASE\NG LTLSQPLHMLNNIYLVRPSDGDWIDITLGQVTPTLYMLSEDRLQW KKLCQVHFAEKQFCRHLIILSEKGHIEWKLMYFALQKHYPKEQY GDTLHFCRHCSILFWKDSGHPCATAADPDSCFTPVSPQHFIDLFK F
6956	8605	3839	QTSTSIFASPTSPPVLGESVLDQNSFDLNNNGSDAEQEEMETQSS DFPPSILTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVS PEISPEVCPAASTVSPAVFSVVSPPASSAVLPAVSLEVPLTASV TSPKASPVTPAAFPATSPANKDVSSFLETTADVEEITGEGLT ASGSGDVMRRRIATPEEVRLPLQHGWRRREVRIKKGSHRWQGETW YYGPGCGRKMKQFPEVIKYLSRNNVHSVREHFSFSPRMPVGDFF EERDTPEGLQWVQLSAEIPSRQAIITGKGRGRPRNTEKARTKEV PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI AKSKKKMRQKVORGEQCTTIOGOARNIKRKQETKSLKQKEAKKKS KAEKEKGKTKQEKLKEKVKREKKEVKMKKEEEVTKAKPACKAD KTLATQRRLERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRVP GLTLPSEGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSPSLGVLQEGL LCQGDSLGEVQDLLVRLKAALHDPGFPSPYQOSLKLKILGEKVSEI PLTRDNVSEILRCFLMAYGVEPALCDLRTOPFOAQOPPQOKAAV LAFLVHELNGSTLIINEIDKTLESMSYSRKWKIVEGRLRLKT VLAKRTGRSEVEMEGPPECLGRRRSSRIMEVTSGMEEEEEESI AAVPGRRGRRRDGEV рАТАССIPELERQIEKLSKRQLFFRKLLH SSQMLRAVSLGQDRYRRRYWLPYLAGIFVECTEGNLVPEEVIK KETDSLKVAAHASLNPAFSMCKMELAGSNTTASSPARAGRPRK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPOAQLOPEAQLHAPAQPQPOLOQ LQLQSHKGFLQEGLPSLQGQSHDLSQSAFLSWSLQTSQSHSSL LSSSVLTPDSPGKLDLAPAPSQPPEEPDPEAESSPDPQALWFNI SAQMPCNAAPTTPPAVSEDOPTPSPQQLASSKPMNRPSCAANPCS PVQFSSTPLAGLAPKRRAGDPGEMPOSPTGLQPKRRGRPPSKF FKQMEQRYLTOLTAOPVPEMCSGWWIRDPPEMLDAMLKALEPR GIREKALHKLHNLKHDFLQEVCLRPSSADPFEPRQLPAFOEGIM SWSPKEKTYETDLAVLQWVEELEQRVIMSGLQIRGWTCPSPDST REDLAYCEHLSDOEDITWRGRGREGLAQPKRTTNPLDLAVMRL AALEQNVERRYLREPLWPWTHEVVLEKALLSTPNGAPEGTTIEIS YEITPRJRVWROTLECRSAAQVCLCLGQLESIAWEKSVNKVT CLVCRKGDNDEFLLCDGCDRGCHYCHRPKMEAVPEGDWFC CLAQVGEFCTQKPGPKRGQKRKSGYSLNFSEGDCRRRVLLR SPRAGPRYSEEGLSPSKRRRLSMRNNHSDLTFCIILMEME SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMERLLRGGYTS SEEFAADALLVFDNCQTFNEEDSEVGKAGHIMRRFFESRWEFF YOGKQGCSVQGRWGVTLWHPPTQTKTCHFHLMLPWPVQTQV RYNPDF
6957	82	3514	HLIVAMPEPTKKEENEVPAAPPPPEITSKEKEAGTTPAKDWTLV ETPPGEEQAKQANANSQSLISLFIEKPGGGTVKVGEDITFIAKVA EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVTFEMO IIKAKDNFAGNYRCEVTYKDKFDSCSFDELVHESTGTTPNIDIR SAFKRSGEQEDAGEFLDSGLLKREVKQOEEEPQVDWELLKUN TKPSEYEKIAFOYESPCTSGMLKRLKRSIREEKKSAAFAKILD VYQVDKGGRVRFVVELADPKLEVWKWNKGQELRSTKYI FEDTRCOSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKC EDTTDYCGERVELECEVSSEDDAQVKNFKNGEEIIILVQTRYRIRV ECKKHILIIEGATKADAADYSVMTGGOSSAKLISVDSLKPLKILT PLTDQTVNLGKEICLKCEISENPCKWTKNGLPQESDRLKVVH KGRIHLVIDHALTEDEGDYVFPADAYNVTLPAKVMVIDPPKII LDGLDAQNTVTVIAGNKLRLIEPISGEPPPKAMWSRGDKAIMEG SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK VKVVDFFDPDPVAPTVTEVGDDWCIMNWEPPEADGGSPILGYFIE RKKKQSSRWMRLNFDLCKETTFFEPKKMIEGVAYEVRI FAVNA\I GISKPSPMSRPFVPLAVTSPPPLLTVDSVTDTTVMRWRPPDH GAAGLDGYVLEYCFEGSTSAKQSDENGAAAYDLP AEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYY SOPILVKE IIIEPPKIHSPKHLQTYI RRVGDRLVILVIPFQGKPRPELTWKD GAEIDKQINQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDFK VE TASIDIRIIDRPGPQIVKIEDVWGRNVALTWT TPKDDGNAAIT GTYIQKADKKMSMEWLRVIEHII IEPVHTELVIGNEYY FRRFSEN MCGLSEDATMTKESAVIARDGKTYK NPVYEDFDFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMK NKVAIVDDPRYRMFS NQGVCTLEIRKPS PYDGGTYCCKAVNDLGT VEIECKLEV KVI AQ
6958	274	1663	PRTSRVKTGSGQSSAMD FSVKVDIEKEV TCPI C LE L TEPLSL DCGHSFCQACITAXIK KESVI ISRG E SSCP VCQ TRFQ Q GNLR PNR HLAN I VERV KEV KMS P QEG Q KRD V CE HH G KKL Q I F C K EDG K V IC W V C L S Q E H Q G H O F R T R I N S T D T I I F I R K A E R S H S G K Y D L Q V K V D K F V E TAS ID I R D P G P Q I V K I E D V W G R N V A L T W T P K D D G N A A I T G T Y I Q K A D K K M S M E W L R V I E H I I E P V H T E L V I G N E Y Y F R F S E N M C G L S E D A T M T K E S A V I A R D G K T Y K N P V Y E D F D F S E A P M F T Q P L V N R L C H S G Y M A T L N C S V R G N P K P K I T W M K N K V A I V D D P R Y R M F S N Q G V C T L E I R K P S P Y D G G T Y C C K A V N D L G T V E I E C K L E V K V I A Q
6959	1	1469	SLVHVVEFGRGIEDFPYLFQQLTHCQQRICSVTQAGVQWCDHSS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQPQTGGLNQSSHLSLSSR DYRMLSSFNEWFWOIRFWLPPNVT WTELEDRDGRVYPHPDQLLAALPLALVLLAMRLA FERFIGLPLS RWLGVDRDQTRRQVKPNATLEKHFLLTEGHHRPKEPQISLAAQCGI TLQQQTORWFRRRRNQDRPQLTKKFC EASWRFLFYLSSFVGGLSV LYHESWLWAPVMCWDYRPNQQLTLSCPAADSEA\SYWWYLLELG FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVIH HFVAVILMTTSY SANJLRIGSIVLLLHDSSDYLLEACKMVNYMC YQQVCDALFLIFS FVFFYTRLVLFPTQI LYTTTYESISNRGPF GYYFFNGLMLLOLLHVFWSCLLRLM LYSFMKKGQMEKDIRSDV EESDSSEEAAAQEPQLQKNGTAGGPRPAPTDGPRSRVAGRLTN RHTTAT
6960	387	2068	AKWAREMQE\TRSF\`RGRPDLSLTHSIVR RRYLAHSGRS HLEPEEKQALKRLVEEPLKMQVDEAASREDKLDLT KKGKRPT PCSDEPERKRFRFNSES ESGSEASSPDYFGPAKNCV ASRSHTEP KEENPRA\SKAVEE SDEERQRDLPAORGEESSEEEKGYKGK TRKPKVVKQAPGKASVSRKQAREESEEEAEPVQRTAKKVEGN KGTKSLKESEOESEEEILAQKKEOREEEVEEEEKE EDEEKCDW K PRTRSGNRKSAAREERSCKQKSQAKRLLGDS DSEEEQKEAASSG DDSGRDREPPVQRKSE DRTQLKGKRLSGSSEDE DSGKGEPTA KGSRKXMARLGS TSGEESDLEREVSDSEAGGGP OGERKNRSSKKS SRKGRTSSSSSDGSPEAKGGKAGSGRGE DHPAVMRLKRYIK ACGAHJRN YKLLGSCCSCHKERLSILRAELEALGMCTPSLKGCR ALKEQREEEAAEVASLDVANIISGSGRPRRKTA WNP LGEAAPPGE LYRRTLDSDEERPRFAPPDW SHMRGIISSDGES
6961	340	1646	RPWSSPTM KPNFSLR L RIFN LNCWG I P YLSK HRA DM RRLGDFL NQESFPDL ALLEEVWSE QDFQ YL RQKL SPTYPAAHHFRSGIIGSG LCVFSKHP I QELTQH YTLNGYPMIHHGDWFSGK\VG L LVLHL SGMVLNAYVTHLHAEYNRQKDIYL AHRV A Q A WELA Q F I HHTSKK ADVVL LCGDLNMH PEDLGCCLL KEWTGLH DAYLET RDFKGSEEG NTMVPKNCYVSQ QELKPFPGVRIDYVLYKAVSGF YISCKSFET TTGFDPHRG TPLSDHEALM ATLFVRHSPPQNPSS THGP\AERS PL/MCVCLKEALDGS I LGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAA I LLWTPS VGLV LWAGAFYLFHVQEVNG LYRAQAE LQHVLGRARE A QDLGPEP QLY ALL\LGQEGDRTKEQ
6962	340	1646	RPWSSPTM KPNFSLR L RIFN LNCWG I P YLSK HRA DM RRLGDFL NQESFPDL ALLEEVWSE QDFQ YL RQKL SPTYPAAHHFRSGIIGSG LCVFSKHP I QELTQH YTLNGYPMIHHGDWFSGK\VG L LVLHL SGMVLNAYVTHLHAEYNRQKDIYL AHRV A Q A WELA Q F I HHTSKK ADVVL LCGDLNMH PEDLGCCLL KEWTGLH DAYLET RDFKGSEEG NTMVPKNCYVSQ QELKPFPGVRIDYVLYKAVSGF YISCKSFET TTGFDPHRG TPLSDHEALM ATLFVRHSPPQNPSS THGP\AERS PL/MCVCLKEALDGS I LGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAA I LLWTPS VGLV LWAGAFYLFHVQEVNG LYRAQAE LQHVLGRARE A QDLGPEP QLY ALL\LGQEGDRTKEQ
6963	374	2618	RVTPLI LKLLKKPKTAENQKASEE N EITQPGGSSAKFGLPCLNF EAVLSPDPALI HSTHSLTN SHAHTGSSDCDISCKGMTERIHSIN LHNFSNSV L E T L N E Q R N R G H F C D V T V R I H G S M L R A Q C R C V L A A G S PFFQDKL L LGYSDIEI P S V V S V Q S V Q K L I D F M Y S G V L R V S Q S E A L Q I L T A S I L Q I K T V I D E C T R I V S Q N V G D V F P G I Q D S G Q D T P R G T P E S G T S G Q O S S D T E S G Y L Q S H P Q H S V D R I Y S A L Y A C S M Q N G S G E R S F Y S G A V V S H H E T A L G L P R D H H M E D P S W I T R I H E R S Q Q M E R Y L S T T P E T H C R K Q P R P V R I Q T L V G N I H I K Q E M E D D Y D Y G Q Q R V Q I L E R N E S E E C T E D T D Q A E G T E S E P K G E S F D S G V S S S I G T E P D S V E Q Q F G P G A A R D S Q A E P T Q P E Q A A E A P A E G G P Q T N O L E T G A S S P E R S N E V E M D S T V I T V S N S S D K S V L Q Q P S V N T S I C Q P L P S T Q L Y L R Q T E T L T S N L R M P L T I T S N T Q V I G T A G N T Y L P A L F T T Q P A G S G P K

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			PFLFSLPLQPLAGQQTFTVTSQPGLSTFTAQLPAPQPLASSAGH STASGQGEKPKYECTLCNKTFTAKQNYVKHMVFVHTGEKPHQCSI CWRSESLKDYLK\HMTHTGVRAYQCSICNKRFQKSSLNV\H RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP GARAGPPGVVACTEGTYYVCSVCPAKFDQIEQFNNDHMRMHVSDG
6964	1	178	SGRPFFFFSNTDVYFIKKVTVNRWTAGSSYKMTTRMKSIGKILLQ\QFIG\NCSMFVLVI
6965	757	208	NVFIEPRICGFMTSAHPGQKHPDFSMGLLFPLLAJALEVCSCGS SGSLGYNLPONH\GLLGRNTLVLQGMRRISPFLCKDRSDRFPQEKVEVSQLOKA\QAMSFLYDVLQVNFNSHKALL\CCMEHDL PGPTPHFTSSAAGTPGDLGAGDGRRSWGQWVIEGSTLALRRY FOESISTLE
6966	820	1867	IITALGVRCMPGCPGCPFGCMAGPRLFLTALALELLGRAGGSQPA LRSRGATACRLDNKESESNGALLSGERLDTWICSLIGSLMVG LSGVFPILLV\PLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL HLLPEAWAYTCASAPGEGQSLQQQQQLGLWVIAGILTFLALEK /HVPGQOQGGDQPGPQQRPHCCRAQWRPLSGPAGCRARPRCR GP\DIKVSCYLNLLANTIDNFTHGLAVAASFLVSKKIGLTTMA ILLHEIPHEVQDFDRWSAAKLQLSTALGGLLGAGFA ICTOSPKVEETAAWVLPTSGGFLYIALVNVLPDLEEDPW
6967	162	633	GFLPFKWWILDLSASSRMETDCNPMEISSLMSGFEGSELNGFEG TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK ERNRYCIELTEAGLKVN\GYAFDQVDDHLLQTPYHETVYSLDTL\ SPAYREAFGKR\LLQRLFEALKRKGQS
6968	3	2265	RGGGGRRGGPGARERERPGEPERTMEEAAGGRGCFOPHPGLOKTPA QFHLLSSMSSLGPPAFAFSARWAQEA\YKESAKEAGAAA\VPAPV PAATEPPPVHLPAIOPPPVLPGPFFMPSDRSTERCETVLEGE TISCFVVGKEKRLCLPQILNSVLRDFSLQQINA\VCDELHIYCSR CTADQLEILKVMGIL\LPFSAPSCGLITKTD\AERL\CNALLYGGAYP PPKKELAASLALGLESRSVRVY\CFGKCKG\LVPELYS SPAACIQCLD\CRLYMPPHKVWHSHKALENRTCHWGF\DSA\ NWRAYILLSDQDTGKEEQARLGR\CLDDVKEF\DYGNKYKRRVP RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS LGCVHPRQLSAFRPSPAVSASEKELSPHILP\ALI\RSFYSYKS FETAVAPNVALAPPAQQKVVSPPCAA\VSRAPEPLATCTQPRX RKLTVDTGAPETLAPVAAPEEDK\DSEAEVEVESREFTSSLSS LSSPSFTSSSSAKDLCSPGARALPSAVPDAAPADAPSGLEAEL EHLRQALEGG\LDTKEAKEKFLHEVVKM\RVKQEEKLSAALQAKRS LHQELEFLR\VAKKEKL\REATEAKRNLRKEI\ERLRAENEKKM\KEA NESRLR\KRELEQARQARVCDKGCEAGRLRAKYS\QI\EDLQV\KL QHAEADREQLRADILREREAREHLEK\VV\ELQEQLWPRARPE AAGSEG\AAELEP
6969	1855	118	AGTMHGRLKVKTSEEOAEAKRLEREQKL\LYQSATQAVFQKRQA GELDESVLELTSQI\LG\NAPDFATLWNCRREVLQQ\LETQKSPEEL AALVKAELGFL\ESCLRVNP\KSYGTVH\HRCWLLGR\PEPNWTREL ELCARFL\EVDERNFH\WDYRRFVATQAAV\PPAEELA\PTDSLITR NFSNYSSWHYRSCLLPQLH\PPQD\SGPQ\GR\LPEDVLLKEELVQN A\FTDPNDQSAW\YH\RL\GRADPQ\DA\RL\CHV\SR\EA\CLTV\SF SRPLL\VG\SR\MEI\LLM\VV\DD\SLI\VEWRT\PD\GR\N\RP\SH\W\LC\DL\ AASLNDQLPQ\HT\FR\VI\WTAGDV\K\ECV\LL\K\GR\QEG\W\CR\D\ST\T\DE QLFRCELSV\K\ST\VLQ\SELES\CK\ELQ\E\LE\PE\N\K\W\CL\LT\I\I\LLM RALDPL\I\VE\K\ET\LO\Y\Q\O\T\LK\AWD\PK\R\AT\Y\LD\DL\RS\K\FL\LE\NS VLKMEYAEV\RL\H\LA\H\K\DL\T\VL\CH\LE\Q\LL\VV\T\H\LD\SH\N\RL\RT\L PP\AL\A\LR\CL\ED\PP\PP\RT\VLQ\AS\DN\AI\ES\LD\G\VT\NL\PR\Q\ELL\ CNNR\LOO\PA\VLQ\PL\AS\CP\RL\VL\LN\I\Q\G\N\PL\C\Q\AV\G\I\LE\O\A\ELL\ PSV\SS\VL\T

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6970	?	1528	SFPPLSSPSAVGEGKVAAPCPGRSECARAKMAYIQLEPLNE GFLSRISGLLLCCRWTCCRCCQKCYESSCCQSSEDEVEILGPPA QTTPPWLMASKSSDKDGSVHTASEVPLTPRTNSPDGRRSSSDTS KSTYSLTRRJSSLESRRPSSPLIDIKPIEFGVLSAKKEPIQPSV LPRTYNPDDYFRKFEPLHYSLDNSNDDVDSLTDEEILSKYQLGM LUIFSTQYDLLHNHLTVRVIARDEADLPPPISHGDSRQDMAHSNPYV KJCLLPDQKNSKQTGVYRKTKPQPVFEERYTFFEIPFLEAQRRILL LTVDVDKFSRHCVIGKVSVPCEVDLVKGHHWWKALIPSSQNE VELGELLLSLNLYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI QLVHGLKLVTKTKTSFLRGTDIPFYNESFSFKVPQEELENASLV FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRMLNTHRT AVEQWHSLSRAECDRVSPASLVE
6971	37	3702	ACFYVPGSRSFKLIPRHHGLVNMGRSGKLGSGVSAKLKRWKGHS SDSDNPACRHRQAARSRRFSRPSGRSRSRDLTVDAVKLHNELQSGSL RLGKSEAPETPMEEEAAELVLTEKSSGTFLSGLSRSDCTNVTFSKVQ RFWESENAAHKEICAVLAAVTEVIRSOQGKETETEYFAALIRKA AOHGVCSVLKGSEFMMFEKAPAHPPAISTAKFCIQEIEKSGGSK EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA CAMQAFHSLFHARPGLSTLSAELNAQIITALYDVPSENDLQPL LAWLKVMEKAHINLVRILQWDLGLGHLPRFFGTAVTCLLSPHSQV LTAATQSLKEILKECVAPHMADIGSVTSSASGPQSVAKMFRAV EEGLTYKFHAAWSSV1QLLCVFFEACGROAHPVMRKLCQSLCDL RLSPHFPHTAALDOAVGAAVTSMGPEVVLQAVPLEJDGSEETLD FFRSLWLPVIRDHVQETRLGFFFTYFLPLANTIKSKAMDLAQAG STVESKIVYDTLOWQMWTLLPGFCCTRPTDVAISFKGLARTLGMAI SEKPDLRVTVCOALRTLITKGQCAEADRAEVSRAFKNFLPILFN LYGOPVVAAGDTPAPRRAVLETIRTYLTITQVLNSLLEKASEK VLDPASSDFTRLSVLDLVVVALAPCADEAAISKLYSTIRPYLESK AHGVQKCKAYRVLVEEVCAVSPQGPGALFVQSHLEDLKKTLLDSRS TSSPAKPRPLKCLLHIVRKLSAEEHKEFITALIPEVILCTKEVSV GAKNAFAALLVEMGHAFRLRGFSNOEAEALQCYLVLYPGLVGAVT MVSCSILALTHLLFEFKGLMGISTVEQLLENVCLLLASRTRDVV KSALGFIKVAVTVMVDVAHLAKHVQLVMEAIGKLSDDMMRRHFRMK LRLNFT\KFIPK\FGILTGWKKAVGPKEVHRVLVNRKAEARAK RHRALSQAEEEEEQQEPAQKGKGSIEEILADSEDEEDNE EERSRGKEORKLARQRSSRAWLKEGGGDEPLNFLDPKVAQRVLA TO\CPGGRGRKDHFSFKVSADGRLLIIREADGNKMEEEEGAKGED EEMADPMEDVIIRNKKHQKLHQKEAEEEELIIPPOYQAGGSGI HRPVAKKAMPGAEYKAKKAKGDVKKGRDPDYAYIPLNRSKLNRR RKKMKLOGQFKGLVKAQRGSSQVGEKRNRRKDRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAQORGRARSAEGRIPSSQSPP PAEAGGATRSPPPRPPRPARPPGFSAPPILLRSDAGPGATVSAAA AAATERRRAGATMGAQLSTLGHMVLPPVWFLYSL1LMLKFQRTSP AITLESPPDIKYPLRLDREIIISHTDRRFRFALPSQHILGLPVG QHILYLSARIDGNLVRVPYTPISSDDKGFGVDLVKVFKDTHPK FPAGGKMSQYLESMQIGDTIEFRGPGSGLLVYQGKGKFPAIRPDKK SNPIIRTVKSGVMIAGGTGITPMLOVIRAIMKDPDDHTVCHLLF ANCTEXDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYQGQG\ FVNEEMIRDHLPPP\EEPLVLMCGGPPPMIQQYACLPNL\DHVGH PTERCFVF
6973	1	1964	LOFRCAHRLRAQKCGRPAPGVDAVLCPVIGKLLHKRVVLSA SPRRQEILSNAGLRFEEVPSKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRQADPVVIGADTIVTVGLILEK\PDVKQDAY RMLSRFE\SCREHSVFTGVAVIHCSSKDHQLDTRVSEFYETKV KFSELSSEELLWEYVHSGEPMKDAGGYGIQALGGMLVESVHGDFL NVVGFPLNHFKQLVLYPPRPEDLRRSVKHDSTPAADTFEDL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SDVEGGGSEPTQRDAGRSRDEKAEAGEAQATAEAECHRTRETLP PFPTTRLELIEFGFMLSKGLLTACKLKVPDILLKDEAPQKAADIAS KVDASACGMERLLDICAMGLLEKTEQGYSNTETANVYLASDGE YSLHGFIMHNNDLTWNLFNTYLEFAIREGTNOHHRALGKKAEDLF QDAYYQSPETRRLRFMRAMHGMTKLTAQVATAFNLRSRFSSACDV GGCTGALARELAREYPRMCVTVFDLDPDIIELAAHFQPPCPQAVQ JHFAAGDFFRDPFLPSAELYLICRILHDWPDDKVKLLSRVAESC KPGAGLLLVETDEEKRAVQALMOSLNMLVQTEGKERSLGEY QCLLELFGFHVOVQVHGVLDAILVPPKWPPEAACSL
6974	3082	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK LLAARPGLGTYKQATMVYKTLFALCILTAGWRVQELPTSAPLSV SLPTNIVPPPTIWTSPONTADATASFSNGTHNSVLPVTASAP TSLLPKNISIESREEEITSPGSNWEGTNTDPSPGSSTSGGVH LTTTLEEHSLGTPEAGVAATLSQSAEPPTLISPOAPASSPSS STSPEVFSASAVTINHSSTVSTQPTGAPTAPESTPEEESSDHT PTSHATAEPVPVQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCWKALKLETAMETLINVFHAAHSGKEGDKYKLSKKE KELLTELSGFLDVKEML*ATEALKTPEEA*KSPIIQCSSRS SLPPAQOPPPYL*LSAVPVTIHLPLPPLLPPQAQKDVAVKVMK ELDENGDGDEVDFQEVYVVLVAALTVCACNNFFWEN
6976	1216	970	GCQL*VAYGTTENSPTVFAHPPEPDTEOKAESVGRIMPTEARI MNMEAGTLAKLNTPGELCIRGYCVMILGYWGEPOKTEEAVDQDKW YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH PKVQEYVQVVGVKDDRMGEIACACIRLKDGEETVVEEIKAFCKGK ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ ACPGRLA
6977	1296	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDOKGKLKTPDFA*R ANKKSKHHVNGNRTVEPFFEGTQMAVFGMGCFWGAERKFVWLKG VYSTOFGAGGYTSNPTYKEVCSEKTGHABEVVRRVYQPEHMSFE ELLKVFWENHDPTQGMROGNDHGTOYRSAIYPTSAKQMEAALSS KENYQKVLSEHGFCPITTDIREGQTYYAEDYHQOYLSKNPNGY CGLGGTGVSCPVGIIK
6978	3	242	SFPFRDSRRCGCKGSSLRHTAVAMVKSKEAKCRLCOLFKGSQ FAIRWGFIPLVYIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAAAIALSRRCRHWSGPFFPSPPDRKGLRGTEPWE AGPGSGATGARAMDVRLLKVNELREELQRRLGTLRGLKTELAE RLQAALAEAEPPDDEREDADDEPGRPGHINEEVETEGGSELEG AQPPPPGLOPHAEPGGYSGPDPGHYAMDNITRQNOFYDQVQIKQE NESGYERRPLEMEQQQAYRPEMKTEMKGQAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPAAEEDDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVXKHLPSTEPDPHVVRIGWSLSDCSTQL GEEPFSYGYGGTGKKTNSRFENYGDKFAENDV1GCFADFECGN DVELSFTKNCWGMIAFRQKEALCGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHPLSERIRGTVGPKSKAECIEIMMV GLPAAGKTTWAIAKHAASNPSSKKYNNILGNTNAIMDKMVRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDOTNVYGSQAQR RKMRPTEGFORKAIVCPTDEEDLKRTIKRTDEEGKJVDPHAVL EMKANFTLPVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGFGRGGGGFORYENRGPGGNRGGFONRG GSGGGGNYRGFFNRSGGGGYSQNWRGNNRDNNSNNRGSYNRA PQQOPPPQOPPPQOPPPQOPPPQOPPPQSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPQSFQGFFSTFQPSYSQOPPYNQGGYSQ GYTAPPFFFFPAYNYGSYGGYNPAPYTPPPPTAQTYQPQPSY NQYQQYIAQQWNYQQWNPYQWPPYYGNYDGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRRGTMQKLQTRSPAMSLSDPGLGYHPT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CWTLRWPPLCSLHALHVFHLCFSSRLGTPVSPRLAMDPCNSCEA GGSCACAGCKCKCCTSKKSCCCPLGCAKCAQGCICKGA SEKCSCCA
6981	10	1054	PGRGFRRASLRPAAFAARGVFQGGLGQAKOARTRACAALPTPHPS APRLLEPGQVFPSLFPFFFFPWPWNMLTKAQYDEIAQCLVSVPP ROSLRKLIKORFPPSOSQATLLSIFSQEYCKHIKRTHAKHTSEAJ ESYYQCRYLNGVVKNGAAPVLLDLANEVYDAPSLMARLILERFLO EHEETPPSKSIIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL VDCIKHAIKHEHEVLLRDLLEKKNLSFLDEDQLRAKGYDKTPDF ILQVQPVAVEGHIIHWIESKASFGDECISHAYLHDQFWSYWNRFG PGLVIIYWGFIQELDCNRERGILLKACFPTNIVTLCHSIA
6982	153	1285	FPQODCSAPAAPGLAGSEPRRLRAYRRRQRARGLKRVANLAPP PSLLQGLQGWAQAPVQDGTLCPEDSRSASSPMIQNSRPSLLOPODV GDTVETMLHPVLCGSISGTCSTLLFQPLDLKTRLQTLQ PSDHGSRRVVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPVGVI YFGTLYSLKQYFLRGHPPTALESVMLGVCSRSGVCMSPITVI KTRYESGKYGYESIYAALRSIYHSEGHRLFSGLTATLLRDAPP SGIYLMFYNQTKNIVPHDQVDAFLIPITNFSCGIFAGILASLVT QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIIPRA LRRTLMAAMAWTIVYEMMAKGLKS
6983	82	773	EMSFLQDPSFFTMCMWISIGAGALGAAALALLANTDVFLSKPOK AALEYLEDIDLKTLKEPEPTRFKAKELWEKNGAVIMAVRRPGCFL CREEAAADLSSLKSMLDQLGVFLYAVVKEHIRTEVKDFQPYFKGE IFLDEKKKFYGPQRKMMFMCGFIRLGWVNFFRAWNGGFSGNLE GEGFILGGVPVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI KPQTLASEKK
6984	1845	1282	GGRSAYSALPAGSLPRVPATAAKMASGQVQVADEVCRIFYDMKVR KCSTPSEEIKKRKKAVIFCLSLADKKCIIVEEGKEILVGDVGVTIT DPFKHFMGLPEKDCRYALYDASFETKESRKEELMFFLWAPELA PLKSKMIIYASSKDAIKKKFQGIKHECQANGPEDLNRCIAEKLG GSLJVAPEGCPV
6985	1887	1324	RRTAGIYPCFPKPGRTRHACSVVLLIITGOLAFFDFQESCAMM WQKYAGSRRSMPMLGARILFHGVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHIPEAQEALGPPLNIIHYLKLIDRENFDIVDAKLK IPVSGSKSEGILLYVHSRGGPFQRWHLDEVFLELKDGQQIPVFK LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKESLADQDFKMYIAF VFKEKKKKSALFEVSEVIQVMTNNYEEINILKGVRDSSYLESSL ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC LLFSRWESEDEPFRPVQAKXFEEFHGDYEKQFLHVLRSRKDKTGIV VNNPNQSVFLIDROHLLQTPRNKATIFKLCSCICLYLPQEQLTHW AVGTIEDHLPYMPPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPOKSQRYYMYNTAC FLGEIEVGLYTIQILQLTPFFHKENELSKHHMVQFLSGKWTIPP DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYVLLKMRYTO KEIAEIMSLKKVSRCKRKYTELFCFLDPCLLQSKESQLQBEENC RKKLEALRADRFAGLLEYLPNPKDATTMESIVNEYAFLLQQNS KKPMTNEKQNSILANIISLCKPKNSKLIQPLTTLKKQLREVLQF VGLSHQYGPYFLACLFWPNQELDDOSKLIIEKVSSLNRSFR GQYKRMCRSKQASTLFLYLGKRGKGLNSIVHKAKIEQYFDKAQNTN SLWHSGDVWKKNEVKDLLRRLTGQAEGLISVEYGETEKKIPV ISVYSCPLRSGRNIERVSFLGFSIECPPGL
6988	3	689	TQLLRRPAVFVGSAAASGIRSGLWSASSGHWCAPAAAGRAHAPVPR LVRGLGAASTAAPQDAQTPQPMRADC1MRHLPYFCRGQVVRG FGRGSKOLGIPTANFPEQVVDNLPA DISTG IYYGWA SVGSDVH KMVVSIGWNPYYYKNTKSMETHIMHTFKEDFYGEILNVAIVGYL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RPEKNFDLSLESLISATIQGDIIEAKKRLELPEHLKIKEDNFFQVS KSKIMNGH
6989	2	1116	LMPSDRPLSPSTTHASAGSHCHAPPTTARRAFPIPIPQGSKSNMATL KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLAEL ALVDVIEDKLKGEMMDLQHGSLSFLRTPKIVSGKDNYNTANSKLV IITAGAROQEGESRLNVLQVNVNIFKFIIPNVVVKYSPNCKLLIV NPVDILTYVAAWIKISCFPKNRVIGSGCNLDSARFRYLMGERLGV HPLSCHGVLGEHGDSSPVWSGMNVAGVSLKTLHDLGTDKDK EOWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR RVHPVSTMIKGLYGIKDDVFLSVPCLILGQNGISDLVKVTLTSEE EARLKKSAADTLWGQIKELQF
6990	719	258	THASGMASVVLNLTRTAVTSSLSPPTPATALAVRYASKKSGGSS KNLGGKSSGRROGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV GKNKCLYALEEGIVRYTKEVYVPHPRNTZAVDLITRLPKGAVLY KTFVHVVPAKPEGTFKLVAML
6991	169	453	RRSSDFHNPGLSRPVSLSRENIIHHQVICSTKKNRKNPKKIAVLL SSLLMTNLPNESTENQPVDAFTLQDFELTYACVEGTGCLF CGRHVH
6992	944	510	RQAPGCSLALRCVRQVYCGLVRAPQVQTRPLSSRFVERRGALY RSPMNQENPPYPGPGPTAPYPYPQPPQPMGPQPMGGPYPPPCGY PYQGYPQYWGQGGPQEPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLWDMLT
6993	1	374	QWCVTCPOHNARCGPAVPPGJQAYGAAPPEDLQVDFTEMSKRCG DRVWIKNWNVASLCPWKGPQTVVLSPPATAVKEGIPAWIHHSH VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSLPGKHFVFKAILMLVLAVALIHLHSALACSE RDFAPPGQQKREAPVDVLTOIGRSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISSAISVAFALSGIAAQLNNAALGLAGDYLIAQGLKLS PGOVQTFLWGGAGALVVVWLLSLLLGLVIALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLALLLYIALSRLTGSRASGAQL EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQQCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQI EHEAGTQLHRQTGLLLGMKNEQELKTIQANLSRORVEHQCLSS EELKQRFNIRLPRGEVGLLDNSSGGVIYAYKALRALQDAIRQLG GIVRDEGEVKVVEINPGLLTVKTTSRSYQAKSLVITAGPWTNOLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIDGVQIL SSFVRDHLPLDKPPEAVIESCMYNTNPDEQFILDRHPKYDNIVI GAGPSGHGFKLAPVVGKILYELSMKLTQPSYDLAPFRISRFPSLG KAIIL
6996	543	1942	ETANAEAAAARKSAMDWKEVLRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGRKNTNEFYKTIPRFYIPLPAENEVLLQKLR EESRAVPLQRKSRELLDNEEQLNLWFLDKHQTPPMIGEAMIN YENFLKVGKAGAKCKQFFTAKVFAKLLHDTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDENYIILEIPTLPQL DGLEKSFYFSYVCTAVRKFFFLLDPLRTGKIKIQDILACSLFLDD LLELRDEELSKEQETNWFSAPSALRVVGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFOECLTYDGEDYKTYLDFVLALEN RKEPAALOYIFKLLDIENKGYLNVFSLNYYFRAIQLEMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTILIDL NGFWTYENREALVANDSENSADLDDT
6997	370	2104	AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPPYFLVRF TVIYNECMASKKRELFSNLQEFAGPSGKLSLLEVCCGTGANFKF YPPGCRVTCIDPNPNFKEFLIKSIAENRHLQFERFVVAAGENMH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QVADGSVDVVVCTVLVLCVKNQERILREVCRVLRPGGAFYFMEH VAAECSTWNYFWQQQLDPAWHLLFDCNCNLTRESWKALERASF LKLOHIQAPLSWELVPHIYGYAVK
6998	2	616	FVSRALLRVRSSRRHPPAERAAPGRPEDAPIECPGATNCPEPLWC SHLPVPYAPPTMESRGKSASSPKPDTKVPOVITTEAKVPPAADCK APLTKPSKKEAPAEKQOPPAAPTTAPAKTSAKADPALLNNHSN LKPAPTPVSSPDATPEPKPGDGAEDEAASGGPGGRGPWSCEN FNPLLLVAGGGVAVAIAIALLIICGVAFLVRKK
6999	14	1591	GRAGACSSRRDTAMSIEESSDVIRLIMQYKENSILHRALATLQE ETTVSINTVDSIESFVADINSGHWDVTLQAIQSLKLPDKTLIDL YEUVVLELIELRELGAARSLLRQTDPMIMLKQTOPERYIHLENL LARSYFDPREAYPDGSSEKEKRAAIAQALAGEVSVVPPSRIMAL LGQALKWQHQGLLPPGMDTDLFRGKAAVVDVEEKKPTQLSRH IKFGQKSHVCECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL KYQAQDNFMMDAVALCMCFSRDTMELATGAQDGKIKVWKIQSG QCLRRFERAHSKGVTCLSLFSKDSSQILSASFQDTIRIHGLKSGK TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKITTECS NTFKSLGSGTAGTDITVNSVILLPKNPEHVVVCNRNSNTVVI MNMQ GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV TGKLERLTLTVHEKDVGIAHHPHQNLIAITYSEDGLLKLWKP
7000	2	827	GPGVVVFELMESEGPPESERSEEFFSQREEEEEEAEPEETGP KNPILQPALTGVEGLCKIFEDPENPPIHEQAMOLLEEDI VGRN LILYAAACMAGOSDVIRALAKYGVNLNEKTRGYTLIHC ETLKALVELVDVIEALNFRERARDVAARYSQTECEVFLDWADA RLTLKKYIAKVSIAVTDTEKGSGKLLKEDKNTIISACRAKNEWL ETHTEASINELFEQRQLEDEVTPIFTKMTTPCQVSAKS DQKRSQDDTSN
7001	2056	844	RRCLJIAFLKGCFIFIFYFIFETEFLSCCPGWSAVAQSRLIAN FASQVQAOQPKDSQVGPDKVSEAAPKRALYESVFGSCEICGP TSPKRCLCIRPSEPVDAVVVSVKHDPLPLLPEANGRSTNSPTI VSFAIVSPTQDSRPNSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKEYPESRICRLFDGTEPIVLDLSLQ HYFIIDRGQMFRYILNFRTSKLLIPDFFKDYTLIYEAKYFQL QPMILLEMERWKQDRETRGFRPCECLVVRVAPDLGERITLSDK SLIEEVFPEIGDVICNSVNAGWNHDSTHIVRFPLNYCHLNSVQ VLERLQORGFEIVGSCCGGVDSQQSEYVLRRELRTPRVPSVI RIKQEPDL
7002	1043	498	PMPSSTRWTTSTYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHSQRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPAATPPSKPGAPAHPCASSRHLAHLAPSSPGLPA RGAEVVC
7003	618	61	QGRFRACFWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKD GKOGKVQVQIRQRNWVVGGLNTHYRIGKTMDYRGTMPSEAP LLHQVQLVDPMDRKPTEJEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNPPCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\YYCRVRPLGFPDQECCIEVINNTVQLHTE GYRLNFRNGDYKETOYSFKQVFGTHITQKELFDVVAANPLVNDLIIH GKNGLLFTYGVTSQGKTHMTGSPGEGGLLPRCLDMIFNSIGSF QAKRIVVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPPFDPINPNLHLNLCPVKIKHNHNMYVAGCTEVEVKSTEAEFE VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNL



SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL AEDPOELRKGFOHPARLVKFLVGMKGKDEAMA1GGHWSPSLDGP DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA AAAAAAAATGTEAGPGTAGGSENGSEAAQPAGLSGPAEVGPGA VGERTPRKKEPPRASPGLAEPPGSAGPQAGPTVPGSATPME TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER NAKAEEKKLPPPPPQAPPEEENESPEEPGVVEGAAFQSRLPH DRMTSQEAAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQ LTFEATLQQLEAPYNSDTVLVHVRVHSYLERHGLINFGIYKRIKPL PTKKTGKVIIGSGVSGLAAARQLOSGMDVTILLEARDRVGGRV ATFRKGNVYADLGAMVVTGLGGNPMAVVSKQVNMLAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLTEATSYLSHQLDFNVLNNKP VSLGQALEVVVIQLOEKHVKDEQIEHWKKIVKTQEEELKELLNKMV NLKEKIKELHQYKEASEEVKPPRDIRTAELVKSKHDLTALCKE YDELAETOGKLEEKLOELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWQDDDFEFTGSHLTVRNGYSCPVVALAEG LDIKLNTAVRQVRYTAGCCEIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPPLFEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLKAPILLALVAGEAAG IMENISDDVIVGRCLAIKKGIFGSSAVPQPKETVSRWRADPWA RGSSYVAAGSSNDYDLMQPIPGSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA AAAAAAAATGTEAGPGTAGGSENGSEAAQPAGLSGPAEVGPGA VGERTPRKKEPPRASPGLAEPPGSAGPQAGPTVPGSATPME TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER NAKAEEKKLPPPPPQAPPEEENESPEEPGVVEGAAFQSRLPH DRMTSQEAAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQ LTFEATLQQLEAPYNSDTVLVHVRVHSYLERHGLINFGIYKRIKPL PTKKTGKVIIGSGVSGLAAARQLOSGMDVTILLEARDRVGGRV ATFRKGNVYADLGAMVVTGLGGNPMAVVSKQVNMLAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLTEATSYLSHQLDFNVLNNKP VSLGQALEVVVIQLOEKHVKDEQIEHWKKIVKTQEEELKELLNKMV NLKEKIKELHQYKEASEEVKPPRDIRTAELVKSKHDLTALCKE YDELAETOGKLEEKLOELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWQDDDFEFTGSHLTVRNGYSCPVVALAEG LDIKLNTAVRQVRYTAGCCEIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPPLFEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLKAPILLALVAGEAAG IMENISDDVIVGRCLAIKKGIFGSSAVPQPKETVSRWRADPWA RGSSYVAAGSSNDYDLMQPIPGSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPOEGSLARIPTSLDCLENTLGVEEQRHETSDHEAEPD CIISSEAPTSPLGHLTSEYDTRNSYQDEDTAGGPPRSPGVWEWEM PLATDSDPTSDPTEVNGIISQSPQVPPHNPLOKSOQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQQLTLQKPVPLYRGS SVSASRUVKPRQSSPQLHNLASYTKKHTSSVYJISERLEMKPG PQAQGLVMEAATHSQGDGSTDLSKLTQQLIEFEKSLAGPGTEP DKILRHFISIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKAPPPLVVRPSRPAPLPPSAQQRTNAV SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLRIEEME RDLDOMYSRAQEELNLMLEEKODESSRAETLEDLKFCESNIESLN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIC ELLQTERDYIIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMIV IKVSKQLLAALEISDAVGVPFLGHHRDELEGTYKIVCQNHDEAIA LLEIYEKDEKIQKHLQDSDLADLKSLYNEWGCTNYINLGSFLIKP VORVMRXPULLMELLNSTPESPKDVKPLTNAVLAVKEINVNINE YKRRKDVLVKYRKGEDDSIMKISKLNHISIKKSNRVSLLKHK LTGFAPQIKDEVFEETEKNFRMQRERLIKSPFIRDLSSLYQHRES ACVKVVRAVSMWDVCMERGHDRDLEQFERVHRYISDOLFTNFKER TERLVIISPLNQLLSMFTGPHKLVQKRFDKLDFYNCTERAELKL DKKTELLEQSLARNNYEALNAQLLDELPKFHQYAQGLFTNCVHG AEAHCDFVHQALEQOLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ QLQVFTFFPESLPLATKPKFERKTIDRQSARKPLLGLPSYMLQSE ELRASLLARYPPEKLFQEAERNFNAACDLDVSLLLEGDLVGVVICKK DPMGSQNRLWLDNGVTKGFWYSSFLKPYNPRFHSADAVGSHSS TESEHGSSSPRFPRQNSGSTLTFNPNS\MAVSGFTSGSCQKOPQ DASPPPKEDWDQGTLASALNPSNSESSPSRCFSDPDTSQPRSGD SADVARDVKQPTATPRSYRNFRHFEIVGYSVPGNGQSQDLVKG CARTAOAPEDRSTEPDGSEAEQGNQVFAVYTFKARNPNELSVSA NQKLKILEFKDVTGNTTEWNLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVSQSLRVWQVGPVARERVIPFSSLL GFRRCVSCVAGSAFSCPRLASASRSNGQGSALDHFLGSQPD SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRLRVVLLGAPNAG KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDT G1SPGKQKRHHLELSLLEDPWKSMESADLVVLLVDVSDKWT QLSPQLLRCLTKYSO1PSVLVMNKVDCLKQKSVLLELTAALEG VUNGKKLKMROAFHSHPGTHCPSPAVKDPNTQSVPNORIGWPH FKEIFMALSALSQEDVKTLCQYLLTQAQPGPWEYHSAVLTQTP EICANIIREKLLLEHLPQEVPYVNVQOKTAVWEEGPGGELVIQQKL LVPKESYVKKLICPKGHV1S1QAEAGHDLMDIFLCDVDIRLSV KLLK
7016	167	2513	ILNAPKPPPFRDSVEAAVAKRTDGGGSWGTGMDVSGQETDW AFRQKLVSQIEDAMRKAGVAHKSSKDMESHVFVFLKAKTRDEYLS LVARLI1HFRDI1HKKSQASVSDPMNALQSLTGGPAAGAGISM PPRGPGQSLGGMGSLGAMQPMMSLQGQPPPSTGMAHPSMAVVS TATPQTOLQLQOVAAAAATARSSSSRRYSSSSSSNSKQ FOAQOSAMOO\QFOA\VVQQQQQLQQQQQQQQQQQQQQQQQQ QIQQQQQQQLQRIAQOLQLQQQQQQQQQQQQQQQQQQQQ PMQQPQPPPSQALPQQLQQMHTQHHQPPPPOOOPPVQAQNQPSQ LPPQSQTQPLVQSAQALPCOMLYTOPPLKVFVAPMVQQPPVQ OQQQQQTAVOTAQAAQMVAPGVQVSQSSLPMSSPSPGQQVQ OSMPPPPDOPSPGOPSSQPNNSVSSGPAPSPFSPSPSPQ \QSPVTARTPONFSVPSPGPLNTPVNPSSVMSPAGSSQA EQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSL LDILTDPSKRCPLTQKCEIALEKLKNDMAVPTPPPPVPP TQQYLQCP LLDAVLANIRSPVFNHSLYRTFVPAWTAIHGPPI TAPVVC TRKR RLEDDEOSIPS1VQGEVARLDPKF1VNLDP SHCSNN GTVH LIC KLDKDKLPSVPPLELSVPADYPAOSPLWIDROWYD ANPFLQSV HRCMTSRLQLPDKHSTALLNTWAQSVHQACLSAA
7017	1	1785	INLGNTCYMNSV1*ALFMATDFRRQVLSLNINNGCNSLMKKLQHL PAFLAHTQREAYAPRIFFEASRPPWFTPRSQDCSEYLRFL LHEEEK1LKVQASHKPS EILECSETS1QEV AASVKA VLTET PRTS DGEKTLIEKMF CGKLRTH IRCLNCR STSQKAE AFTDLSLAF WPS YSLEYMS CPDCS OSPS I QDGGL M QASV PGP SEEP VV N PT AA F ICDSL LVNE K TIG S P N E F Y C E N C A S L Q A E K T M Q I T E P Y L I L T L R F S Y D Q K Y H V R R K I L D N V S L P L V L E P V K R I T S

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
			FSSLSESWVDFTDLENLAKKLKPGSTDEASCTKLVPPYLLS SVVVHSGISSESQHYSYARNITSTDSSYQMYHQSEALALASSQ SHLLGRDSPSVAEQDLENKEMSKEWFLNDSRVTFTSFQSVQK ITSRFPKDVTAYVLLVKKQHSTNGLSGNNPTSGLWINGDPPLOKE LMDAITKDNLKLYLQEELNARARALOAASACSFPRPNGFDDNDP PGSCGPTGGGGGGGFTNTVGRLLV
7018	484	1066	SLVFRGNTWSEAGAHHCASFNLNAAHOLFVGTERIRAPEIIFQ PSLIGEEQAGIAETLQYILDRYPTPKDVCQEMLVQNVFLTGGNTMYP GMKARMEKELEMMPFRSSFPQVQLASNPVLDAYGARDWALNHL DDNEVWIRTRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA QASSKSSAAGGGGAGEQAA
7019	1046	335	APGGFLVTMVFPAPSPPPWMLGCCSHEVTAGPPTLCKDMSALVA RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDKNGRS SSGALRGVCSCVEAGKACDPAARQFTNLIPWCLPHTGNRHNHWA GLYGRLEWDGFFSTVTMPEPMGKGGRVLIHPEQHRVVSVERCAR SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK ARESASAKIKEEEAKD
7020	1	2154	FADSCKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR NGFLMRKVAVFFSNTPTRASPQQLREAVLKLSDAGITPLFLTRQE DROLINALQINNTAVGHALVLVPLAGRDLTDFLENVLTCHVCLDIC NIDPSCFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF NEMKKYIAYLVRQLDMSPPDKASQHAFARVAVVQHAPSEVDNAS MPPVKVEFSLTDYGSKEKLVDLFLSRGMDTQLQGTRALGSAIEYTI ENVFESAPNPRDLKIVVLMLTGEVPEQOLEEPAQRVILQAKCKGY FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR FGRLLPSFVSSENAFYLPDIRKQCDWFQGDQPTKNLVKFGHKQ VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTKPVTTKPVTT INQPSVKPAAKPAKPAKPVAAKPVATKIAVRPPVAVKPATAAK PVAAKPAAVRPPAAAAKPVATKPEVPRPOAKPAATKPATTKP MVKMSREQVQFITEITSAKLHWERPEPFGPYFYDILTVTSADQS LVLKQNLTVTDRVIGLLAGQTYHVAWCYLRQVATYHGSFS TKKSQPPPPQPARSASSSTINLMVSTEPALTETDICKLPKDEG TCRDFILKWWYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVIVSMGT
7021	2	338	VNAVSFFPQNGYAFATGSDDATCRLFLRADQELLLYSHDNIICG ITSVAFSKSGRLLLQAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS CLGVTDGGMVAATGWSWDFLRIWN
7022	2	856	VYIGCSFWSHPLIPDNRKLFEAEQDLDLFRDIDQSLPRNAALRKL DLIKRARLAKVHAYIISLLKEMPSVFGKDNKKELVNNLAEIY GRIERHQIISPGDFPNLKRMDQLQAQDFSKFQPLSKSLLEVDD DMLAHDIAQLMVLVRQEESSQRPIQMVKGGAEGFTLHGPGFGHGYG EGAGEGIDDAEWVVARDKPMYDEIPTLSPVDGKITGANAKKEM VRSKLPLNSVLGKIKWLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRVAE
7023	2	748	AMVFGGVVPPVQYRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMILLMLKLCTEVRVANELNARRRSF TAADSKDEEVKVAAPRSFLDFPHFWQWSSFSDVQCVLAFTG VAGYITYLSJDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCCLLQVLVDLA ILGQAYAFARHPQKPAHVAHPTGTAKL
7024	1207	190	RTGVTGVVAQVWMFGGGVLSSGEQLQMPVKPERGLGPGSDGLV SSRRGSPGTVLGLPFWLLTPVLSRSRISRSMLLLTSRPTAWHRLS QLKPPVLPGLTGGQALHLRSWLLSRRQGPATGGQQPQGPGLRT RLLITGLFGAGLGGANLALRAEKERLQQQRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPD1CPCDELEKLVQV VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TGCTKQVAQASHSYRVVYNAQPKDEDQDYIVDHSIAIYLLNPDG LFTDYYGRSRSAEIQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNENL-K\HSDLCLCFRGDWEGNTQFQTLQDNQEECF KQVIRTCERKPTFNQHTVFNHLQRQLNTGDKLNEFKELGKAFISG SDHTQHOLIHTSEKFCGDKECGNTFLPDESEVIQYQTVHTVKKTY ECKECGKSFSLSSLTGHKRHTGEKPFCKDCGKAFRFHSQLS VHKRHTGEKSYECKECGKA
7026	328	1146	NPNPSIEDIKDIIKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG LHQALLSVGVSKRSNTVVGNEERGTPYASRPFKDMNPNALEK SSVLRHCCDLIGLVAAGSSDKICTSSLVQVRRFKAMMASIGRLS HGESADLLISCNAESAIGWISSRWPVGLMFTFLGDFESPLHK LRKSS+LPRKHR+QPINAVRMFLDQCMDGSIALRAIVSEIPVFE EKKQNG+KGIGEIF+VWGCTLPPHYWGAFTTNVPKLSNSGKLLG QDEOPHIFG
7027	43	954	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH YYQELKIVPEGENGQFMDALREPLPATLRITGYKSHAKEILHCL KNKYKFLVQEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK SPELEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD MCAAPGSKTTQLEMIHLADMNVPFPEGFVIANDVDNKRCYLLVH QAKRLSSPCIMVVNHASSIPLRQIIVDGRKEILFYDRILCDVP CSDGDTMRKNIIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRFPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSRNFI KKMOSWYMSLSPTYKQRNEDPRKLFSKLPEAERLIVDYSCLQR EILLOGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA KLIPNAIQ
7029	1343	40	VLESNTTEAKQATGTSSKLRHGTGQEKGRGPRCPGGLAQLRLWG /PCPHAGRETGPRASAPIPGS+GHGHW+RKDGRGERSEGPSAL SPHSPSLLNMQQAPTHVPGPGMSQPRSSVVPQGVGVGSOLSR RWRA+RSLPGAAASERTEMKERSP/RPCOGYDSSNWFQPGKK TRKRNSRRTNTMVSRGCGCLLYPLQSIMPE*QLR*GAHASPTQG R*GKGGPRSLTKASGTTIPTPFFGS1P/RPTRDGPGTDNS\ AAPGQKRGHREA*QGPPEV/WGRVTTHLOGPAG*TKPLGS\RN VPGPAEGQEGAGLEGRP+PLKGCRTSLTFSPQLS1PMVGKKP PEGTTASFFF\RSCHSE*RKPPPSCPHAFALSLPHPLPLPPL PLFLPGACT\HSARSGRPGQSETGSLCHNCHCPCPKCSPGG T
7030	2	521	FVCFSAPGSGQGGKRRVNMELEAVGERVFAAEALLKRRIRKGRM EYLVWKWKGWSQKYSTWEPEEN1LDARLLAAFEEREREMELYGP KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIYPGRSPQDL ASTERAREGLRN\RVCPQRQAAPAPAAP\PRRGPSGPGPRPG+G PGL+FPGPQPGPSKHGFPVASEQHQHQHQLPRRGPGPGP RPG
7031	960	59	HCSVPGAEWPRKPFQAQICPQLTSRPHLSSPRSLSPCGHSPGP /CKPS/RHCDDELHEGPSSRTAALPCGKPKQPKHGVEECG/PCPC A PRLTEPPALTVSFVGRAAPSGAL*PSCKACSCASCHRLAPEAAL SAAAPRPSLGSQONASGLPAAASLPPQDSSOPHKTVPSPARSVPP IGAQARAAPPRLWCPRALVSG+EASPEAVSVAAGPPVPGPTP STSGSTASHSRGRC*SPR*TPA\PRRDHGRSAAFEVITA ASQGGPRPTGAGRTPSPLGLPPFSRGPPAASARPFCRHP SL
7032	1393	2104	RRPGRTEPVEPPPVPVPPRASNSKSCR*RNLLHLAPL*QSPLRK SRO1GTSSLPPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL EPWMKRCQFGRHLHSLFWKSWQKMSFLLTPKLDTSIMSGWRYRQR LPRLHTFLKKSLQMASELAPPPTPAPLASSLPPP PLA+LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP EHCWVLPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSPKRAATPLDSGP GP*APPGPSSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMMPSSCPWRITGALGPSAGSRALGRCTSSVGPGSRWLTRTSSP GCATRTWRTMRMPEPRPLRSRGMESAPGIPAEPLPSALPSGPAPS AAAPSAPPTPAAAGPNTL*SRRTAEWCWPPSCCCWGWC*SWSA WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS SSSTCPTRSRSDRGAAWTP/SPMGAPLLPCSVPLISREEALQDPR NPSP*GVCSSGSSGHAGLALGKPPVACSV
7034	92	1942	EDTSSMPFRLLIPGLCALLPOHHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAFPFDELRLPTCDGHDWTGSFS1TLIDALD TLL\TLYFQIILGNVSEFQRVVEVLQDSVDFD1DVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVCTAGIGTFIVEFATLSSL TGDPVFDVARVALMRLWESRSDIGLVGNHIDVLTGKWWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVSMPVFOSEAYWPGLOSILGDIDNAMRTFLNYY TVWKQFGGLPEFYNIQPGYTVKEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVCECGFATIKDLRDHKLDNRMESF FLAETVKVLYLLFDPTNF1IHNNGSTFDAVTPYGECLGAGGYI FNTEAHPIPDPAALHCCORLKEEQWEVEDLMREPYSLKRSRSKFQ KNTVSSGPWEPPARPGTLPSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLAIKK K
7035	92	1942	EDTSSMPFRLLIPGLCALLPQHHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAFPFDELRLPTCDGHDWTGSFS1TLIDALD TLL\TLYFQIILGNVSEFQRVVEVLQDSVDFD1DVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVCTAGIGTFIVEFATLSSL TGDPVFDVARVALMRLWESRSDIGLVGNHIDVLTGKWWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVSMPVFOSEAYWPGLOSILGDIDNAMRTFLNYY TVWKQFGGLPEFYNIQPGYTVKEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVCECGFATIKDLRDHKLDNRMESF FLAETVKVLYLLFDPTNF1IHNNGSTFDAVTPYGECLGAGGYI FNTEAHPIPDPAALHCCORLKEEQWEVEDLMREPYSLKRSRSKFQ KNTVSSGPWEPPARPGTLPSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLAIKK K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAHLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAHLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRDRQLRQAFEEIIL QYNKLLEKSDLHSLVLAOKLQAEKHDVPRNHEISPCHDGTWNNDNQ LOEMAQLRIKHQEELTELHKRGELAQ\,RVIDLNQNMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERAACRSSKGTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRDRQLRQAFEEIIL QYNKLLEKSDLHSLVLAOKLQAEKHDVPRNHEISPCHDGTWNNDNQ LQEMAQLRIKHQEELTELHKRGELAQ\,RVIDLNQNMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERAACRSSKGTSRTG
7040	34	789	KITPPRPHRCSSGHGSDNSSLGELPPAMGKTAFLYHSGGSS GYESVMRDSEATGSASSAODSTSENSSVGRCRSLKTPKKRSN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PGSQRRRLIPALSLDTSSPVKPPNSTGVRWVDPGLRSSPRGLGEPFEIKVYEIDDVERLORRRGGASKEAMCFNAKLKILEHRRQRIAEVRAKYEWLMLKELEATKQYLMMDPNKWLSEFDLQEYVWELDSLEYALECCTERLESRVNFCKAHLMMITCFDIT
7041	2	567	SGRVAMGRRRAPAGGSGLGRALMRHQQTQRSRSHRHTDSWLHTSELNDGYDWGRNLNLSQVTEQSSLLDDFLATAELAGTEPVAEKLNJKFVPAEARTGLLSFEESQRIKKLHEENKQFLC1PRRPNWNQNTTPEELKQAEKDNFLEWRROL\VRLEEEQKLILTPFERNLDFWRCOLWRVIERSDIVVQIVDA
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGALPLETVTMYTVIPKSKYVLUVKPDTQYPPYSENLDLFKRLAENSASNDDLLMAEVSDYGDKLTLEREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD EKGRYKRPHGAFSGGSFAGYFNTVGSKEGWTPTSTVSSRQNRAD KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR OLAATAAPIGATLDDDLITPAKLSVGSELLRKMGWKEGOGVGP RVKRRPRRQKPDGVKIYGCALPPGSSSEGSEGEDDDYLPDNVTFAPKDVTVPDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG SERAGDLGEIGLNKGRLKGISGQAFGVGALEEDDDIYATETLS KYDTVLKDEEPGDGLYGTAPRQYKNQKESEKDLRYVGKILDGF SLASKFLSSKKIYPPPELPRDYPYRPMVAATSENSHLLQV LSESAGKATPDPGTHSKHQLNASKRAELLCETPIQGSATSVLEF LSOQDKERIKEMKQATDLKAAQLKARSILQAQSSRAQPSAAA AGHCSWNMALGGGTATLKASNFKPKFAKDPKQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGRERDEPAAALLYASSHSTLSSRF THAKEEDDSQVEVPRDQENDVGDQSAVKMKMFGKLTRDTFEW HPDKLLEFO/RLVGLPFRVKRDYKSVFNFLLTPETASLPTTOASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPK QQSPLVNUKEEEHAPELSAN
7044	276	734	EVYLTDEFAKGRKVADLYELVQYAGNNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNQYLLQCTRNIIPDEG EPTDEETTGDISSDMFDVLLNFAEMNKLWVRMHQGHRSRDRERQERQELRILVGTNLVRLSQV
7045	3	513	LGFKMEALSRAQQEMSIAALKQHDPIITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRNMLVEPVNK DLEFQLHEPFLLYRNASLSIYISIWFYDKNDCHRIAKLMADVVE ETRRSQQA/RSGQTESQPGQWLQRQPAHRHPGDAEQSQG
7046	3	513	LGFKMEALSRAQQEMSIAALKQHDPIITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRNMLVEPVNK DLEFQLHEPFLLYRNASLSIYISIWFYDKNDCHRIAKLMADVVE ETRRSQQA/RSGQTESQPGQWLQRQPAHRHPGDAEQSQG
7047	103	486	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSSKKALDTAISLGPHSYER
7048	92	627	FFCLTLSSWDYRHHATRRISSPVFTMEDSGKTFSSSEEEANY WKDLAMTYKQRAENTQEEELREFQEGSREYEAELETQLQQJETRN RDLLSENRLRMELETIKEKFEVQHSEGYRQ1SALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHXHEAKRAVREL NNYEIRPGRLGVCCSVNDNCRLLFIGGIPKMKKREELEELIAKVT EGVLVDIVYASAADKMKNRGLRRLGVREPPRGCHWLGRKLIAWXASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VPFVEAVGRIYELRLWMDFDGKNGRYAFVMYCHKHEAKRAVRELNNYEIRPGRILGVCCSVNDNCRLFIGGIPKMKKKREEILEEIAKVT
			EGVLDVIVYASAADKMKRNGLRLRGVREPPRGCHWLGRKLIWGXASSLWG
7051	119	816	KKMNLAIEICDANKKGREYALLGNYDSSMVVYQGVMOOIORHCQS
			VRDPAIKGKWQQVRQELLEEEYEQVKSIVGTLESFKIDKPPDFPV
			SCQDEPFRDPAWPPPVPAAEHRAAPPQIRR/RQSRSKTSEERNGR
			SRSPGTCRSTP/PISEKCPSTS RDKDVRARGRDKGRKRNQDG
			ASDGEMPKFDGAGYDKD\LEALERDIVSRNPSIHWDDIADLEEA
			KKLLREAGVLPMWW
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
			TYRNSMYHNVHKVFKDVKVLDVGSGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
			TYRNSMYHNVHKVFKDVKVLDVGSGTGILSMFAARQGPRR
7054	1	1036	GTSORSRETDAARRSAGAEPТАRLPWPAALEEWPSCPCEPLGPG
			RRCRWDAMEYDEKLAFFRQAHLNPFNKQSGPRQ4EOPGPGEVVD
			VTPEEALPELPPGEPEFRCPEVMDLGLSEDHFSPRVGLFLASD
			VQQLRQAAIEECKQVILELPQEPEQSEKQKDAVVRLIHLRLKLOELKD
			PNEDEPNIRVLLERHRYKEKSKSVKQTCDCKCNTIJIWGLIQTWYT
			CTGCYRCHSKCLNLISKPCVSSKVSHQAEEYELNJCPEGLDSQ
			DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSPHCHWNDLAV
			IFARVVHNWDFEPRKVSRCMSRYLAL\WSRPVLRIREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCFLWLSMNVLFWKTFLLYNQGP
			EYHYLHQMLG/ALCLSRASASVNLNCSLILLPMCRTLLAYLRG
			SQKVPSSRTRRLDKSRTFHITCGATCIFSGVHVAALVNALN
			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
			M
7056	2	527	DSRRVSWRSWLANE/WGKHLCFLWLSMNVLFWKTFLLYNQGP
			EYHYLHQMLG/ALCLSRASASVNLNCSLILLPMCRTLLAYLRG
			SQKVPSSRTRRLDKSRTFHITCGATCIFSGVHVAALVNALN
			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
			M
7057	1368	431	GIYLHVINKEKIPRPTC1GDRQENDKENLNLENHRDOELLHASCOA
			SGEVPSQASLRGFFTEDEPGCGEGENLPEALQN10DEGTGEQL
			SPQERISEKOLGQHLPNPHSGEMSTMWLEEKRETQKGQPRAPM
			AOKLPTCRECGKTFYRNSQLIFHORTHTGETYFOCTICKAKPLR
			SSDFVKHQRHTHTGEKPKCDYCGKGFSDFSLRHHKEIHTGEKP
			YKCP1CEKSFIQRSNFRHQRVHTGEKPYKCSHCKSFSWSSL
			DKHORSHLGKPPQ*PTVTKLSPPISTISQPSH1QNTOLHQEELCLR
			GYC
7058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRA1CCKGPPPAR
			PEYDLVCIGLTGSGKTSLLSKLCSES PNVSTTGPSIKAVPQ
			NAILNVKEGGADNIRKYWSRYYQGSQGVIFVLDASSEDDLEA
			ARN*SC70LQHPQLCTLPFL1A
7059	1	1178	WPAFPQPAAMDALLGTPGRRARGCLGAAGPTSSGRAARTPA
			APWARPSSAWLECVVTFDLELGQALELTVYPNDFR1TDKEKSI
			CYLSFPDSHSGCLGDTOSFMRQCGGQSPWHDADRHYNRAP
			VALOREPAHYFGVYVFRQVKDSSVKGYFQKSLVLSRLPFPVRL
			FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM
			CVVVQVRI PSRVDKSESSPPQFDQENLLPAPVVLASVHELDLF
			RCFRPV1THMOTLWELMLLGEPLLVLVAFSPDVSSSEMVLALTSC
			QPLRFCCDPRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK
			TLOHWPFI1RVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEADGN1EYKKLVNPSQ
			YRFEHLVNTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEEMRAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKTLHRMMAEKVGADITVLREREVDYDSDMPRKITEVLRVKVPDNQQLFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRHLHEIQSGRTSSISFEILGFNSKGEGVHGINGTQWQGQTLRMGW***RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNGVKIKRQGHPGNGNLGPNGNSEGVGRAGRHH*GPWALGQVNVNYSDSRTAEEICESSSKMITFIDLADGHHKYLHTTJFGLTSYCPDCALLLV SANTGJAGTTREHGLALALKVPPFTIVVSKIDLCAKTTVERTVRQLERVLKQPGCHKVPMLVTSEDDAVAAQQFAQSPNVTPIFTLS SVSGESLDLLKFLNILPPLTNSEKEQELMQLTEFQVDEIYTVPEVGTUVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGDPGJ
7061	364	710	ARMPSPGLGPPCLPVMDPETTLEEPETARLKFRGFYCQEVAGPRE ALARLRELCOWLQPEAHSSKEQMLEMILVLEQFLGTLPPPEIQAQWV RGQRPGSPEEEAAALVEGLQHDP*ARMPSPGLGPPCLPVMDPETTL EEPETARLRFRGFCYQEVAGPREALARLRELCOWLQPEAHSSKE QMLEMILVLEOFLGTLPPETQAWVRGQRPGSPEEEAAALVEGLQHDPGQLLG
7062	71	744	AKAGTNLNERLHWLHSYFCIYKHKLKSSQKDKVRFQMACTQAGER TAIYCLTONEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL YGRYKDPDENKIGVDG1IQQFCDDLSLDPASISVLUWKFRAA TOCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDRAFTKFD FYQFTFTFAKNPQKGQLDL*MAGAYWKLVLSGRFKFLYLWNTFL MEHH
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEIDLXAFERR LTEYIHCQLQPATGRWRMLLIVSVCTATGAWNWLIDPETQKVSF PTSLWNHPPFTTICITLIGLFFAGIHKRVVAPSIIAACRTVLA EYNMSCDDTGKLILKPRPHQ*QSSLIVMGLKIAFLRISDTAKSHKGFLRLDM
7064	300	684	RDTGSDPESRTRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS SRRTGCTCPPESGHAQARRSRRASRKGARGAVRSAAARGC SSAGRWRLETPGRRRGPPACAAAAGRRLRGPA*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAAP PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSGRAAAEEAASAAGGRQKGFDRKAWEGRRRTPGGRSQSEPKAPPQKRSEAAFASMAHSFVAVQVFGMNNIADPEELFTKLERIGKGSFGEVFKG1IDNRTQOQVVAIKIIDLEEADEIEDIQQEITVLSOCDDSYVTKYYGSYLGSKLWJIMEYLGGSALDLLRAGPFDEFQ
7066	356	676	PGPQRGPWRAEEGGHPDADHPRAPASLRSNVRAATMMQICDT YNQKHSLPNAMNRFIGAVNNMDQTVMPVSLLRDVPLADPGLDND VGVEVGGSGGCLERTPP
7067	152	973	KENITMATEIGSPPRFHFMPRFQHQAPROLFYKRPDFAQQOAMQ OLTFDGKMRKAVNRKTIDYNPSVIKYLENRIWORDQRDMRAIQ PDAGYNNDLVPPIGMLNNPMNAVTTKEVRTSTNKVKCPVFVVRWTPEGRRLVTGASSGEFTLWNGLTFNPFETILOAHDSPVRAMFTWSHNDMWMLTADHGGYVKYWQSNNNNVKMFQAKEAIAREARFIHNIPFSVPIVMVKLFSKCIILGAEMHGLCQFLGNFLHPIINTIFFVFT HSPFCWAFF
7068	222	816	D7MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMDTDDDDDDDDDDDDDDDDDEDNSLFPTRPRSHFFPFLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLLDLQNNK1KEIKENDFXGLTSYGLI1NNNKLTKIHPKAFLTTKKLRLYLSHNQLSEIPLNLPKSLAELRIHENVKKK1QKDTPKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEEEESQAEQENRDETLAKOTLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSLMPLTPFWTLLQSNVPVLQPLPLEMPPPPPPPPESPPPPPPPPAPKMPPP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
			EVTKKGRKDKAKKS <sup>KT</sup> KMPSLVKKWQSIQRELDEEDNSSSEEDRVSTAQKKIEEWKQQQLVSGMAERNANFEA.
7070	1	547	DGTMDSEAVQKATALIEQRLAQEEENEKLRGDAQOKLPMDLLVLEDEKHHGCAOSAALQKVKGQERVKRTSLDLRREIIDVGGIQNLIELRKKRKCKKRKDALAASHEPPPPEPEEITGPVDEETFLKAAVEGKMKVIEKF <sup>L</sup> ADGGSADTCQFRR <sup>T</sup> ALHRSLEGHMEILEKLLDNGATVDFO
7071	2	921	ARGTLRALETAKKVGKV <sup>G</sup> ANGOKAAGPSADS <sup>V</sup> TENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQYFQDPRTQI <sup>P</sup> FEV <sup>P</sup> QV <sup>P</sup> Q <sup>T</sup> GYYPPPPTV <sup>P</sup> AGV <sup>A</sup> PCV <sup>P</sup> RFVRSNNVPESSI <sup>P</sup> PASMPYADH <sup>Y</sup> STFS <sup>P</sup> RDRMNSSPYQ <sup>P</sup> PPPQ <sup>P</sup> Q <sup>T</sup> YGPV <sup>V</sup> PPVPSGMYAPVYDSRRIWRPMYQRDDII <sup>I</sup> RSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPP <sup>S</sup> E <sup>P</sup> RTTVPLPREPCGHLKT <sup>C</sup> EEQ <sup>Q</sup> IRRKP <sup>D</sup> QWAQYHTQ <sup>A</sup> KPLV <sup>S</sup> STLPVATQSPT <sup>P</sup> STLN <sup>R</sup> GE <sup>G</sup> S
7072	2	921	ARGTLRALETAKKVGKV <sup>G</sup> ANGOKAAGPSADS <sup>V</sup> TENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQYFQDPRTQI <sup>P</sup> FEV <sup>P</sup> QV <sup>P</sup> Q <sup>T</sup> GYYPPPPTV <sup>P</sup> AGV <sup>A</sup> PCV <sup>P</sup> RFVRSNNVPESSI <sup>P</sup> PASMPYADH <sup>Y</sup> STFS <sup>P</sup> RDRMNSSPYQ <sup>P</sup> PPPQ <sup>P</sup> Q <sup>T</sup> YGPV <sup>V</sup> PPVPSGMYAPVYDSRRIWRPMYQRDDII <sup>I</sup> RSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPP <sup>S</sup> E <sup>P</sup> RTTVPLPREPCGHLKT <sup>C</sup> EEQ <sup>Q</sup> IRRKP <sup>D</sup> QWAQYHTQ <sup>A</sup> KPLV <sup>S</sup> STLPVATQSPT <sup>P</sup> STLN <sup>R</sup> GE <sup>G</sup> S
7073	50	504	LAHGSFGVSDFPAPAAA <sup>A</sup> PAHTLTSFGSLS <sup>P</sup> QFRKPLGRAPAMP <sup>A</sup> LVR <sup>V</sup> RK <sup>V</sup> V <sup>I</sup> LG <sup>C</sup> YRCV <sup>G</sup> K <sup>T</sup> SLA <sup>H</sup> OF <sup>V</sup> VE <sup>G</sup> E <sup>F</sup> SE <sup>G</sup> Y <sup>D</sup> PT <sup>V</sup> ENT <sup>T</sup> YSK <sup>I</sup> V <sup>T</sup> L <sup>G</sup> K <sup>D</sup> E <sup>F</sup> L <sup>H</sup> L <sup>V</sup> D <sup>T</sup> AG <sup>Q</sup> DE <sup>I</sup> S <sup>L</sup> P <sup>Y</sup> S <sup>F</sup> I <sup>I</sup> GV <sup>G</sup> Y <sup>V</sup> L <sup>V</sup> SV <sup>T</sup> SLH <sup>S</sup> FQ <sup>V</sup> I <sup>E</sup> S <sup>L</sup> Y <sup>Q</sup> K <sup>L</sup> H <sup>E</sup> G <sup>H</sup> Q <sup>K</sup>
7074	263	1003	VCPVLCSTROQEPGHSSLV <sup>T</sup> YFGKP <sup>T</sup> TRKEFLLGH <sup>C</sup> IAAGKMNISVDLETNYAELVLDVGRV <sup>T</sup> LG <sup>E</sup> NSRKKMKDCKL <sup>R</sup> KQQNERV <sup>S</sup> RAMCALLNSGGGV <sup>I</sup> KA <sup>E</sup> IENEDY <sup>T</sup> KDGIGLDL <sup>E</sup> NSFSNILLFVPEYLD <sup>F</sup> MQNGNYFLIFVKWSLNTSGRLITTLSSNLYKRDITSAKV <sup>M</sup> NATAALEFLKDMKKTRGR <sup>L</sup> YLRPELLAKRPRVDI <sup>Q</sup> EENN <sup>M</sup> KALAGVFFDRTELDRKEKL <sup>I</sup> FTESTH <sup>V</sup> EI
7075	598	1005	NYINFFFRKEYPPHVQ <sup>V</sup> K <sup>E</sup> INPVRLS <sup>L</sup> R <sup>L</sup> Q <sup>G</sup> V <sup>E</sup> R <sup>I</sup> M <sup>K</sup> T <sup>E</sup> E <sup>S</sup> Q <sup>V</sup> E <sup>P</sup> E <sup>I</sup> K <sup>R</sup> K <sup>V</sup> Q <sup>K</sup> R <sup>H</sup> C <sup>T</sup> Y <sup>Q</sup> P <sup>T</sup> P <sup>L</sup> S <sup>P</sup> A <sup>K</sup> K <sup>C</sup> L <sup>T</sup> H <sup>L</sup> E <sup>D</sup> L <sup>Q</sup> R <sup>N</sup> C <sup>R</sup> Q <sup>A</sup> ITL <sup>N</sup> E <sup>S</sup> T <sup>G</sup> P <sup>L</sup> L <sup>R</sup> T <sup>S</sup> T <sup>I</sup> H <sup>Q</sup> N <sup>S</sup> GGQ <sup>K</sup> S <sup>Q</sup> NT <sup>G</sup> L <sup>T</sup> T <sup>K</sup> F <sup>Y</sup> G <sup>N</sup> N <sup>V</sup> E <sup>K</sup> V <sup>P</sup> I <sup>D</sup> I <sup>I</sup>
7076	279	1049	LOSESSNAAEGNEQRHEDDEQ <sup>R</sup> S <sup>K</sup> R <sup>G</sup> GS <sup>W</sup> K <sup>G</sup> R <sup>K</sup> R <sup>K</sup> P <sup>L</sup> R <sup>D</sup> S <sup>A</sup> PK <sup>S</sup> P <sup>L</sup> T <sup>G</sup> Y <sup>V</sup> R <sup>F</sup> M <sup>N</sup> E <sup>R</sup> Q <sup>E</sup> L <sup>R</sup> A <sup>K</sup> R <sup>P</sup> E <sup>V</sup> P <sup>F</sup> P <sup>E</sup> I <sup>T</sup> R <sup>M</sup> L <sup>G</sup> N <sup>E</sup> WS <sup>K</sup> L <sup>P</sup> <sup>E</sup> E <sup>K</sup> ORYLDEADRK <sup>E</sup> RYM <sup>K</sup> KE <sup>L</sup> E <sup>Q</sup> Y <sup>Q</sup> K <sup>T</sup> E <sup>A</sup> Y <sup>V</sup> F <sup>S</sup> R <sup>K</sup> T <sup>Q</sup> D <sup>R</sup> Q <sup>G</sup> K <sup>K</sup> SH <sup>R</sup> Q <sup>D</sup> A <sup>R</sup> Q <sup>A</sup> T <sup>H</sup> E <sup>K</sup> E <sup>T</sup> V <sup>K</sup> ER <sup>V</sup> F <sup>D</sup> I <sup>I</sup> F <sup>T</sup> E <sup>E</sup> FL <sup>N</sup> H <sup>S</sup> K <sup>A</sup> R <sup>E</sup> A <sup>E</sup> L <sup>R</sup> Q <sup>L</sup> R <sup>K</sup> S <sup>N</sup> M <sup>E</sup> F <sup>E</sup> ER <sup>N</sup> AA <sup>L</sup> Q <sup>K</sup> H <sup>V</sup> E <sup>S</sup> M <sup>R</sup> T <sup>A</sup> E <sup>V</sup> K <sup>L</sup> E <sup>V</sup> D <sup>V</sup> I <sup>Q</sup> E <sup>R</sup> S <sup>R</sup> NT <sup>V</sup> I <sup>D</sup> Q <sup>H</sup> L <sup>E</sup> T <sup>L</sup> R <sup>Q</sup> V <sup>L</sup> T <sup>S</sup> S <sup>F</sup> A <sup>M</sup> PL <sup>P</sup> E <sup>X</sup> G <sup>E</sup> T <sup>P</sup> T <sup>V</sup> D <sup>T</sup> I <sup>D</sup> SY <sup>M</sup>
7077	3	1119	SSMGSNSEINGL <sup>A</sup> R <sup>K</sup> T <sup>D</sup> K <sup>Y</sup> G <sup>F</sup> L <sup>G</sup> G <sup>S</sup> Q <sup>S</sup> G <sup>S</sup> L <sup>K</sup> S <sup>S</sup> I <sup>P</sup> V <sup>D</sup> V <sup>A</sup> R <sup>Q</sup> ELK <sup>W</sup> L <sup>D</sup> N <sup>M</sup> F <sup>N</sup> S <sup>W</sup> D <sup>K</sup> W <sup>L</sup> S <sup>R</sup> F <sup>Q</sup> V <sup>K</sup> L <sup>R</sup> C <sup>R</sup> K <sup>G</sup> I <sup>P</sup> SSL <sup>R</sup> A <sup>K</sup> W <sup>Q</sup> Y <sup>L</sup> S <sup>N</sup> SKELLE <sup>Q</sup> N <sup>P</sup> R <sup>K</sup> FEELER <sup>A</sup> P <sup>G</sup> D <sup>P</sup> K <sup>W</sup> L <sup>D</sup> V <sup>I</sup> E <sup>K</sup> D <sup>L</sup> H <sup>R</sup> Q <sup>F</sup> P <sup>F</sup> H <sup>E</sup> M <sup>F</sup> A <sup>A</sup> R <sup>G</sup> G <sup>H</sup> Q <sup>Q</sup> D <sup>L</sup> Y <sup>R</sup> I <sup>L</sup> K <sup>A</sup> Y <sup>T</sup> I <sup>Y</sup> R <sup>D</sup> E <sup>G</sup> Y <sup>C</sup> Q <sup>A</sup> Q <sup>P</sup> V <sup>A</sup> A <sup>V</sup> L <sup>M</sup> H <sup>M</sup> P <sup>A</sup> E <sup>Q</sup> A <sup>F</sup> W <sup>C</sup> L <sup>V</sup> Q <sup>I</sup> C <sup>D</sup> K <sup>V</sup> L <sup>P</sup> G <sup>Y</sup> S <sup>A</sup> G <sup>L</sup> E <sup>A</sup> I <sup>Q</sup> L <sup>D</sup> G <sup>E</sup> I <sup>F</sup> F <sup>A</sup> L <sup>L</sup> R <sup>A</sup> S <sup>P</sup> L <sup>A</sup> H <sup>R</sup> H <sup>L</sup> R <sup>Q</sup> R <sup>I</sup> D <sup>P</sup> V <sup>L</sup> Y <sup>M</sup> T <sup>E</sup> W <sup>F</sup> M <sup>C</sup> I <sup>F</sup> A <sup>R</sup> T <sup>L</sup> P <sup>W</sup> A <sup>S</sup> V <sup>L</sup> R <sup>V</sup> W <sup>D</sup> M <sup>F</sup> C <sup>E</sup> G <sup>V</sup> K <sup>I</sup> I <sup>F</sup> R <sup>V</sup> A <sup>L</sup> V <sup>L</sup> R <sup>H</sup> T <sup>L</sup> G <sup>S</sup> V <sup>E</sup> K <sup>L</sup> R <sup>S</sup> C <sup>Q</sup> G <sup>M</sup> Y <sup>E</sup> T <sup>M</sup> E <sup>Q</sup> L <sup>R</sup> N <sup>L</sup> P <sup>Q</sup> Q <sup>C</sup> M <sup>Q</sup> E <sup>D</sup> F <sup>L</sup> V <sup>H</sup> E <sup>V</sup> T <sup>N</sup> L <sup>P</sup> V <sup>T</sup> E <sup>A</sup> L <sup>I</sup> E <sup>R</sup> E <sup>N</sup> A <sup>Q</sup> L <sup>K</sup> K <sup>W</sup> R <sup>E</sup> T <sup>R</sup> G <sup>E</sup> L <sup>Q</sup> Y <sup>R</sup> P <sup>S</sup> R <sup>R</sup> L <sup>H</sup> G <sup>S</sup> RAI <sup>H</sup> E <sup>E</sup> R <sup>R</sup> R <sup>Q</sup> O <sup>P</sup> P <sup>L</sup> G <sup>F</sup> S <sup>S</sup>
7078	483	767	FOGQRMAGEQ <sup>K</sup> P <sup>S</sup> N <sup>L</sup> I <sup>L</sup> E <sup>Q</sup> F <sup>I</sup> L <sup>L</sup> A <sup>K</sup> G <sup>T</sup> S <sup>G</sup> S <sup>A</sup> L <sup>T</sup> I <sup>S</sup> Q <sup>V</sup> L <sup>E</sup> A <sup>P</sup> G <sup>G</sup> V <sup>V</sup> F <sup>G</sup> E <sup>L</sup> E <sup>L</sup> AN <sup>V</sup> Q <sup>E</sup> L <sup>A</sup> E <sup>G</sup> A <sup>N</sup> A <sup>Y</sup> L <sup>Q</sup> L <sup>N</sup> L <sup>F</sup> A <sup>Y</sup> G <sup>T</sup> P <sup>D</sup> Y <sup>I</sup> AN <sup>K</sup> E <sup>S</sup> L <sup>P</sup> E <sup>L</sup> Y
7079	2	376	SVVEFKRP <sup>K</sup> E <sup>P</sup> SG <sup>D</sup> G <sup>E</sup> S <sup>D</sup> G <sup>P</sup> I <sup>D</sup> V <sup>G</sup> Q <sup>E</sup> Q <sup>G</sup> Q <sup>L</sup> S <sup>Q</sup> M <sup>A</sup> R <sup>P</sup> L <sup>S</sup> T <sup>P</sup> SS <sup>S</sup> Q <sup>M</sup> Q <sup>A</sup> R <sup>K</sup> R <sup>R</sup> G <sup>I</sup> I <sup>E</sup> K <sup>R</sup> R <sup>R</sup> D <sup>I</sup> R <sup>N</sup> S <sup>L</sup> S <sup>E</sup> L <sup>R</sup> R <sup>L</sup> V <sup>P</sup> T <sup>A</sup> E <sup>K</sup> Q <sup>G</sup> S <sup>S</sup> K <sup>L</sup> E <sup>K</sup>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AEVLQMTVDHLKMLHATGGTGTHALLFOASFQOQIF
7080	200	595	VQLPLEAPCLSLLSCLRDHSGGNRDLSSRRHHDRCRVYCSQDGIPY LTHPLCHQDVSVGRQLQIRALATPGHTQGHLVYLLDGEPEYKGPS CLFSGDILLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP
7081	213	506	AVTEEEMILNSLSCYHNKLJLAPMVRVGTLPMRLLALDYGADI VYCEELIDLKMIQCKRVRVNEVLSTVDVAFDDRVVFRTCEREQN RVVFQMGTS
7082	3	1137	APSRNTMLMAMCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL CCRSSPRDLRDEGEREHEAAQKAPGAESCPSPPLSISDITGCL SSLENLRLPTLREESSPRELEDESSGQGRCPGTHQGSEDPSMLS QAQSATEVEERHVPSCSTSRRPQAGELILAETGEGETKFKK LFRLNNFGLLNSNWAVPFGKIVGKFPQJLRSSTFGKQYMLRRP ALEDYVVLMKRGTAITFPKDINMILSMMMD1NPGDIVLEAGSGSG GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDWSWKLSH VEEWPNDVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF YPLKHGGVCPVYVNTQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLYLPKSLSRHVSVRTSVVTQQLLSEP SPKAPRPARPCRVSTADRSVRKGIMAYSLLEDLLLKVVRDITMLADK PPFLVLEEDGTTVETEYFQALAGDTVFMVLQKGQKWPQPPSEQG TRHPLSLSHK
7084	3	522	NSVSVSQSRFLASVPGTVGORSAAADMAASTAAGKORIPKVAK VKNKAPAEVQITAEQLLREAKERELELLFPPPQQKIDEEELND YKLKRKRTFEDNIRKRTVISNWKYAQWEESLKEIQRARIYE RALDVDRNITLWLKYAEOMEMKNRQVNHARNIWDRATT
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLYQVYEAIDSRDGASC AELVFSKHPHVANPRLQMASPEEKCCQVLEPPYDEMFAAHLRCT YAVGNHDFIEAYKQTVIVQSFRLRAFOAHKEENWALPVMYAVAL DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR AGIEDSKKWMGLFLVNQLFKIYFKINKLHCKPLIRAIIDSSNLK DDYSTAQRTVYKYYVGRKAMFDSDFKQAEYELSFafeHCHRSSQ KNKRMILYLLPVKMLLGHMPTVELKKYHLMQFAEVTRAVSEG KNNLLHEALAKHEAFFIRCGIFLJIEKLK1ITYRNLFKKVYLL KTHQLSLDAFLVALKEMQVEDVDIDDEVQCILANLIMGHVKGYI SHQHQKLVVSKQNPFPPLSTGC
7086	256	525	ILAARMGKONSKLRPENVMDLLESTDFTEHEIQEWEYKGFLRDCP SGHLSMEEFKKIYGNFFPYGDAKSFKAEPVFTFDANGDTIDFR EF
7087	166	723	LSGSSAGKVAAPCVPSPSNHELVPITTEAFLKNNVVDKGE GASRG NTRKSLEDNGSTRVTPSVQPHLQPIRNMVSRTMEDSCEDL VYVTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHPTPALEKICISICKAMDTWLNAHP HRCRVLHNKG
7088	104	759	GTSAAASPSSLLEMAGEITETGELEYSSYVGLVYMFLNIVGTGALT MPKAFATACWLVLVSLVLLVFLGFMFSMTTFVIEAMAAANAQLHW KRMENLKEEEDDSSTASDSDVLLRDNYERAEKRPILSVQRGS PNPFEITDVRVEMGQMASMFFNKVGVNLFYFCIIIVYLYGDLAIYA AAVPFSIMQVTCSATGNDSCGVEADETKYNDTDRCWGLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRRGGVNFNLNVARTYIPNTKVEC HYTLPPGTMPASDWIGIFKVEAACVRDYHTFWSSVPESTTDG SPIHTSVQFOASYLPKPGAQLYDFRYVNRQGOVCGQSPFPQFRE PRPMDELVTLEEADGGSIDLVVPKATVLQNLQDESQOERNDLM QLKLQLEQVTELRSRVQELERALATARQEFTELMEQYKGISRS HGEITEERDILSROQQDHVARILELEDDIQTISEKVLTKVEELD RLRDTVKALTREQEKLGGQLKEVQADKEOSEAEELQVAQQCENHHL NLDLKEAKSWQEEQSAQAQRLKDVKVQMKDTLGQAOQRAELEP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKZEKCKCWSKERAGLILQSVEAEKDKILK LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN EDATTEDEEAAVGLSCPAALTDSEDES PEDMRLHPMAFVSVETQ ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAAPSRRGVNFLNVARTYIPNTKVECHYTLPPCTMPSASDWIGIFKVEAACVRDYHTFVWSVPESTTDG SPIHTSVQFQASYLPKPGAGAOLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLEEADGGSDILLVUVPKATVLQNLQDESQQERNDLM OLKLOLEGQVTELRSRQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQGHDVARIKELEDDIQTISEKVLTKEVELD RLDRDTVKALTREDEKQLGQLKEVQADKEQSEAEELQVAQQENHHL NLDLKEAKSWQEEOOSAQARLKDVKVAQMKDTLGQAOQRVAELEP LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKKEEKCKCWSKERAGLILQSVEAEKDKILK LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN EDATTEDEEAAVGLSCPAALTDSEDES PEDMRLHPMAFVSVETQ ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEEQLEPWPSPKKARSGRWLNGFKRKMEEF EEPADSGQSLVPVIYSPEYVSMCDSLAKIPKRASMVHSLIEAY ALHKQMRIVKPKVASMEEMATFHTDAYLQHLLQKVSEGGDDHPD SIEYGLGYDCPATEGIFDYYAA1GGATITAAQCLIDGMCKVAIN WSGGWHHAKKDEASGF CYLNDAVLGLI RLRRKFERILYVVDLDH HGDGVEDAFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY YSVNVPIDQDGIODEKYYOICERYEPAPNPGL
7092	522	809	KQGINEDQESQKFRLGECEPPIJSKRQMKKLIKQKOWEEQRELK KQKRKEKRRKKLERQCOMEPNSDGHDRKRVRRDVHSTLRII DCSFDXLM
7093	454	655	NFGVSGVELAQQASMRMSFVIAACQLVLGLLMTSLTESSIONS ECPQLCVCEIRPWPFTPOSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNOSISFFGWWAGSEEPFSFYG DIAFPPLQDYYGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE LLVIRKQOEIDSKDAIILHOFARPNNGVPSLSPFCLKMETYLRM ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLCSDRVILYLVQGEKKVRAPILSQLYFCRYCSELRSLECVSHEVDSHYCPSCLNMPSAEAKLKKNRCANCFCDCPGCMH TLSTRSISTQLPDDPAKTTMKKAYYLACGFCRWTSDRVGMAD KSVGE
7096	224	2067	ETRSLSAQEKPSOAGRRRSSRISFAGALFLTRPLLOELLNNFC SAMSPAPDAAPAPASISLFDLSDADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE OREHYKLWDHRFLNKLQRLKDKPLLSALDFEKQSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVVLGPHQDPPEAEILLQNLQSKGPRDCVVLMAAGHFA GAIFOGREVVTHKTFHRYTVRAKRTAQGLRDARGGPSSHAGAN LRRYNEATLYKDVRLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRTPTFQELQRLVHLKLTLLHVYE EDPREAVRLHSPOTHWKTREERKKPTEEEIRKICRDEKEALGO NEESPKQGSGSGPCEGDFQVEELVEITVGTLDLCSEVLPKRRR RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL LDEAKAPGQPELWNALAAACRAGDVGVLKLQLAPSADPVRVSL LSAPLGSGGFTLHAAAAAAGRSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS FLAAQGDQAFHSGLETNNNSSELPLRVGLKVAQGSPLMGGQVSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSOSHDTMTYC LNKKSPISHEESRLQLQLNKLPCITRPVVLKNSVTOALDVTEQ LDAGVRYVLDLRIAHMLLEGSEKNLHFVHMVYTTALVEDLTLEISE WLERHPREVVIILACRNFEGLSELDLHEYLVACIKNIFGDMLCPRG EVPTLRLQWLWSRGQQIVIVSYEDESSLRRHHELWPGVVPYWWGNRVK TEALIRYLETMKSGR
7098	82	956	SSFLKRCRKVLGCGWCPSEQSLSFSTLEEPFRDKEIDNYCVMPLQT EARSGFWAPNRFPVNICRMTAVDGDGRGSSRETCCRCHFHPSELA LVLLLQDWQPGCGVGICSTSFLGISWALLDYHRLRTCLPSKPLLG LGSSVIFYFLWNILLLWPRVLAVALFSAFFPSVVALHFLGLWLVL LLMWVNLQGTDFFWPDPSSEWLYRVTAVILYFSWFNVAEGRTRGR AIJHFAPFLQLSDSILLVATWVTHSSWLPSGIPQLWLWVCGCGCF LG1ALRLVYYHWHFSCCWKEPDQVD
7099	992	210	LFR LAPGFLRSLARQGYHQIWAFFPLPSGATATWPAASRSRSLA ARSLP RSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPAGD GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC ROSCQMNLLPHLQVQGLTWGHISWDLILALPPODIILASDVFFEP EDFEDILATIYFLMHKPNPKVQLWSTYQVRSADWSLEALLYKWDM KCVHIPLESFDAKDEDIAESTLPGHRTVEMLVISFAKDSL
7100	205	671	ANGGFWEAAGPGEVSPLWVPTASHSKTTALGIGSAPPPLHSLV FLFSFPPQLGDPLEAFPVFKYDRNGLNVSIIECKRVSGLEPATV DWAFLDLTKTNMOTMYESEWGWKDRKREEMTDDRAWYLIWEN SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRAKRLLAGGAVGVWLLVRGVHVSVRAGGGRPRAADMKKD VRILLVGEPRVCGTKTSIMSLVSEEFPEEVPPRAEEITIPADVTP ERVPTHIVDYSEABQSDEQLHQEISQANVICIVYAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVPSR
7102	2	503	WRGGPRAKRLLAGGAVGVWLLVRGVHVSVRAGGGRPRAADMKKD VRILLVGEPRVCGTKTSIMSLVSEEFPEEVPPRAEEITIPADVTP ERVPTHIVDYSEABQSDEQLHQEISQANVICIVYAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVPSR
7103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES LSDKGSELKKSFDAVVFVDVLKVTPEEYAGQITLMDVVPFKAIQP DELSSCGWNKKEKYSSAP
7104	1670	795	RLWEHRSVSAGASGWGLSSPGCLLHPSLPEEERVDILINNAGV MRCPHWTEDEGFFMQGVNHLGEAWAGAAPPVQAOILPRLPPKVL GF*V*VKSDLF11LNPGHFLLTNLLLDKLKASAPSRIINLSSLA HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ GSGVTVNALHPGVARTELGRHTGIGSTFLQHHN\WAJLLAAWS KSPRSWPAPAQHNTLVAEELA\VISGKYFDGLKQKAPAPEAED EEVARRLWAESARLVGLEAPSVERQPLPR
7105	765	143	GOMCRRFSPKSTCCLSMTCCLP/RGLQDPOCLALFRVAVDKHQA LLKAAMSGQGVDRHLFALYIVSRFLHQLQSPFLTQVHSEQWQLST SQIPVQMQHFLDVHNYPDYVSSGGGFGPADDHGCVGSYIIFMGDG MITFHISSKSSTKTDHSRLQHIEDALLDVALSFQAGQHFKRR FRGSGKENSRRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPPRSASRIPFADTH\YSKLQRAFDSIVNKKDHKRMFGT YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYQGQCF GAEFVEVKIDSTFVDKTKLDPNKAYIQTIVFVEPYFDEYEMKDRV TYFEKFNFLRRFMYTTPFTLEGRPRGELHEQYRRTVLTLMHAF PYIKTRISVIQKEEFVLTPIEVAIEMKKKTQLAVAINQEPFD AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL RLCFKEPIMRCGEAVEVNKRSLITADQREYQQELKNNYNKLKENL RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCTQLSQGS
7107	1145	591	*1*WLQTGKKK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSPTLKMFQFVNLSSTFYIAF FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK OTWNNFMEGLGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL QPMNAYGLFDEYLEMIHQFGFTTIVAAFPPLAPLIALLNNIIEI RLDAYKFVUTOWRRSLRAKDIGIWIYGILEGIGILSVITNAFVI AJTSDFIPRLVYAYKYGPGCAGQGEAGQKCMVGYVNASLSVFRIS DFENRSEPSDGSFSGTPLKCYRDRYRDPPHSLVPPGTYTLQFWHVLAW
7109	964	102	WDQKRKRNSLVPGPAGPAQEEPWEKKESLGAQEAALSIQLOPKE TQFFPKSEQVYHLFSVTEGDPPEPKDGSLOPPPIVEVSQVF SEKLADDTSTFEATSEGTLLELQQRNPKAERLRLRWSPAQEEESFRQM VVJHKEIPGKKDHECSECCKTFIYNSHLVVHORVHSGEKPYKC SDCGKTFKQSSNLGQHORIHTGEKPFECNECGKAFRWGAHLVQH CRIHSGEKPYECNECGKAQSQSSYLSQHRIHSGEKPFJCKECG KJ:YGCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHVKPLYDRYRLVKQMLTRASITPVLG SPSTKRRQMLQPIIEGETAHFFEEIKEEEEEDGVNLSSELGDMIL KTAVQVQCSLLKNSSESDVEENQEKLAIDLRLSSRAASMPLELQ LWKARAEKKKLRLKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE YKKIKAKRLLLEVILISKQDSSKSI
7111	2	414	GSGLYRGFTPGGOCIWKPNSMPPDHERNFGFTQFALELNELTAE LKRSLPSSTDTRLRPDORYLEEGNIQAAEAQKRIEOLORDRKKV MEENNIVNHOARFFRRQTDSSGKEWWVNTNTYWRLRAEPGYGNMD GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCVFGNPDIPEVIW FKNDQDIOLEHFSVKEQAKYVMSMTIKGVTEDSGKYSJNJKN KYGGEKIDVTVSVYKGEKIPDMAPPQOAKPKLIPASASAAQG
7113	1	824	KCLRQAWHEAPSSLAFRWSREERAEGGGNLHRSITRDPKPPGLRFSQRPMDKKKKRSPKPCLAQOAPQAPGTLRRRVPPVPTSHGSSL ALGLPHLPSFKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF IJFVTDVYEMEGGLLNLNDFHSGRQIAGFKECSFEQLEHVREM QEKJARLJFSLDVCGEEEDDEEEEEDGVTEGLPEEQQKTMADRNLL DOLLSNLGSC1GALVPGGMRGGEHTYSQSHSWALGEKVGVHGSK SSCPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKJCRKI IYLNTRDFVSVKQRLPKYYSWERCSKHHLNFLGONRSYVRKKDDG CKAYKVLCHYNLKAQPAERFFDPNQRGKALHQKQALRKQSQRS QTGEKLYKCTECGKVFQKANLVLVHQRHTGEKPYECCECAKAF SOKSTLIAHORHTGEKPYECSECGKTFIQKSTLIXHORIHTGE KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ RJETSEKPQCEHNGASDEKPSPKTHWRTHTKENIYECSKCGKS FRCKSHLSVHORIHTGEKPYECSCICGKTFSGKSHLSVHHTHTG EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK SPLKHORIHTGERPECTDCKKAFSRKSTLIXHORIHTGEKPY KCSECCKAFSVKSTLIVHHRHTGEKPYECRDCGKAFSGKSTLIX KHORSHTDKNL
7115	1	947	NAAHGYNNGLWCMYIIPQDWLDRGDESAPIRTPAMIGCSFVVD REYFGDILDPGMEVYGGGENVKLGMRVWQCGGSMEVLPCSRVA HIERTRKPYNNDIYAKRNALRAAEVWMDDFKSHVYMAWNIPM SNPQVDFGDVSERLALRQRLKCRSFVNLLENVYPEMRVYNNLT YGEVRNSKASAYCLDQGAEDGDRAILYPCCHGMSSQLVRYSAADGL LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTORLWD FTQSGPIVSRATGRCLEVEMSKDANFGLRVVQRCSGQKEMIRN NIKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEFWKGYPNIDPTEDPYVT PGSVINNLISINTVREVDHLRDRNSGSSSLNTLPSTSAWSSIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ASNYNVPLSSTAQS TARS NDSKLT WSPGSVTNTSLAHELW KVP LPPKNITAPS RPPPG LFGQK PPLSTWDNSPLR ICGCWGWN SDAF YTPGSSWGE SSSGRIT NWLVLK NLT P QIDGSTLRLTLCM QHGPLJ T FHLNLPHGNALV RYSSK EEEVVAQ KSLHIS DLF LLT L
7117	695	1261	LLISTPGGC E PPPSSIE FTTYTGA WG KALP A P H M F C A F G A L P Q G A F V S Q A A R A I F L L Q P S O A A Q E G L S O P A R A C G A L C S L P W P L R N W G S P I L R L P G G L R T P T N D R K T R T R S A M A C W A R A Q W D T L G P L K L S H R G K V C L R H P R P T G V R G G P G A A G R Q G G M G T R R R G T F T S G A R D P G G L R V K H R C Q P T G H L P
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE E S V L N L G K F H S I V R L V A F C P F A S S Q V A L E N A N A V A S E G V V H E D L R L L E T H L P S K K K V L L G V G D P K I G A A I Q E E L G Y N C O T G G V I A E I L R G V R L H F H N L V K G L T D L S A C K A Q L G L G H S Y S R A K V K F N V R V D N M I I Q S I S L L D Q L D K D I N T F S M R V R E W Y G Y H F P E L V K I I N D N A T Y C R L A Q F I G N R E L N E D K L E E L T M D G A K A K A I L D A S R S S M G M D I S A I D L I N I E S F S S R V V S L S E Y R Q S L H T Y L R S K M S Q V A P S I S A L I G E A V G A R L I A H A G S L T N L A K Y P A S T V Q I L G A E K A L F R A L K T R G N T P K Y G L I F H S T F I G R A A A K N K G R I S R Y L A N K S I J A S R I D C F S E V P T S V F G E K L R Q E V E R L S F Y E T G E I P R K N L D V M K E A M V Q A E E A A E I T R K L E K Q E K K R L K K E K K R L A A L A L A S S E N S S T P E E C E E M S E K P K K K K Q K P Q E V P O E N G M E D P S I S F S K P K K K S P S K E E L M S S D L E E T A G S T S I P K R K K S T P K E E T V N D P E E A G H R S G S K K K R K F S K E E P V S S C P E E A A G K S S S K K K K F H K A S Q E D
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE E S V L N L G K F H S I V R L V A F C P F A S S Q V A L E N A N A V A S E G V V H E D L R L L E T H L P S K K K V L L G V G D P K I G A A I Q E E L G Y N C O T G G V I A E I L R G V R L H F H N L V K G L T D L S A C K A Q L G L G H S Y S R A K V K F N V R V D N M I I Q S I S L L D Q L D K D I N T F S M R V R E W Y G Y H F P E L V K I I N D N A T Y C R L A Q F I G N R E L N E D K L E E L T M D G A K A K A I L D A S R S S M G M D I S A I D L I N I E S F S S R V V S L S E Y R Q S L H T Y L R S K M S Q V A P S I S A L I G E A V G A R L I A H A G S L T N L A K Y P A S T V Q I L G A E K A L F R A L K T R G N T P K Y G L I F H S T F I G R A A A K N K G R I S R Y L A N K S I J A S R I D C F S E V P T S V F G E K L R Q E V E R L S F Y E T G E I P R K N L D V M K E A M V Q A E E A A E I T R K L E K Q E K K R L K K E K K R L A A L A L A S S E N S S T P E E C E E M S E K P K K K K Q K P Q E V P O E N G M E D P S I S F S K P K K K S P S K E E L M S S D L E E T A G S T S I P K R K K S T P K E E T V N D P E E A G H R S G S K K K R K F S K E E P V S S C P E E A A G K S S S K K K K F H K A S Q E D
7120	1991	64	QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTA NL S V V F K D S N S T T P L I F V L S P G T D P A A D L Y K F A E E M K F S K K L S A I S L G Q Q O G P R A E A M M R S S I E R G K W V F F O N C H L A P S W M P A L E R I L I E H I N P D K V I R D F R L W L T S L P S N K F P V S I L Q N G S K M T I E P P R G V R A N L L K S Y S E L G E D F L N S C H K V M E F K S L L S L C L F H G N A L E R R K F G P L G F N I P Y E F T D G D L R I C I S Q L K M F L D E Y D D I P Y K V L K Y T A G E I N Y G G R V T D D W D R R C I M N I L E D F Y N P D V L S P E H S Y S A S G I Y H Q I P P T Y D L H G Y L S Y I K S I P L N D M P E I F G L H D N A N I T F A Q N E T F A L L G T I I Q L Q P K S S S A G S Q G R E E I V E D V T Q N I L L K V P E P I N L Q W V M A K Y P V L Y E E S M N T V L V Q E V I R Y N R L Q V I T Q T L Q D L L K A L K G L V V M S S O L E L M A A S L Y N N T V P E L W S A K A Y P S L K P L S W V M D L L Q R L D F L Q A W I Q D G I P A V F W I S G F F F P Q A F L T G T L Q N F A R K F V I S I D T I S F D F K V M F E A P S E L T Q R P Q V G C Y I H G L F L E G A R W D P E A F Q L A E S O P K E L Y T E M A V I W L L P T P N R K A Q D Q F Y L C P I Y K T L T R A G T L S T T G H S T N Y V I A V E I P T H Q P Q R H W I K R G V A L I C A L D Y
7121	2	546	RPLRPWVLSLGSMVGLMTYGR R Q F S L D T T M R R L I P P F R E A S A K L T T L V D A D A E A F T A Y L E A M R L P K N T P E E K D R R T A A L O E G L R R A V S V P L T L A E T V A S L W P A L Q E L A R C G N L A C R S D L Q V A A K A L E M G V F G A Y F N V L I N L R D I T D E A F K D Q J H E R V S S L L Q E A K T Q A A L V L D C L

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ETRQE
7122	2	546	RPLRPWVLSGSMVGLMTYGRQRQFOSLDTTMRRLLIPPFREASAK LTTLVDADAEAFAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVVASLWPALQELARCGNLA CRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKDO1HHRVSSLLOEAKTQAAVLVDCL ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAAEVSCGSVSGDGAAMRLTPRALCS AAQAAWRENFPPLCGRDVARWFEGHMAKGKKMOSSLKLWVDCIIIE VHDARIPLSGRNPFLQETLGLKPHLLVLNKMDLADLTBQQKIMQ HLEGEGLKVN1FTNCVKDENVKQIIIPMVTTELIGRSHRVHRKENL EYCIMVIGVPNVGKSLNLSLRQHRLRKGKATRVGGPEP GITRAV MSKIQVSEERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL VGEETMADYLLYTLNKHQRFGYVOHVGGSACDNVERVLKSVAV KLGKTQKVLTGTGNVNVIQPNYPAAARDFLQTFRRLGGSVM LDLDVLRGEPRV
7124	2	382	LPLTLLAAPFLAHLPPPQHDDQSPCWHPGPALSPTGLPLSWAM ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS KVFVLESEWGGDSLGLPRDCGSCLLHSAVRSEKGFW
7125	166	1127	NCISEKRNYSFSMOKGKGRTSR1RRRKLCGSSESRGVNESHKSE FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS LFESCLL\RDTRVSYLGYATKWKPPPSFLLA CTFLVSEKH AGHRSLSLEA\YLETLPKAYTCPVCLPEEVNLLPKSLKAKAEEQ RAHVQEFFFASSRDFSSLQPLFAEAVDSIFSYSALLWACTVNT RAVYL\SPGSGNAFLQSRTPVOLAPYLDLNLHSPHVGQVKA AFNE ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH ACVYVSRGWQNQLCS
7126	1	733	CRDMAAFTVPSPARCSQKGSLGHLTQFWLWAAMS PRGQERGT SHSQAREPQRPGRWLLGSLQSSPGTILQAGITASRRRGCMVQRWV QVATGRRAVQVPKGALGLALGETSPGASRGMSGAGGCWALGWA PSPVLPWSLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC WRGGRIASAEAST*TPGSGSRARSRRSPGSRRRSASAPSPTP PTDACA*SCV\RPAGSSRSPRPAAA
7127	1311	277	GLPAMC*KAGYYEETEGDC1PKDR*IEKRFKKEI*RRIPRIF AKOKI*NSOKIGASEIDRGRKEADCSDAAPAARIGAVSVFR RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC ICRST**K*WHOLC*PLSSL*TGLKRRLLL*VLFRI*WLKDCDV *FCQK1FATNFCNWQNLQ*EE*KPVEYSEV*HIMNLLPML* CQSSLRDTIVTWRM*RNYSMFRINNMISSL*DGSIH1PLKLHFY PALIFTLTVPINSCCQRPFLFAHOSIKTLASSGSPMLACLRFL LVKKRAFIHTPRSPGCSV*CKHVLVKDNNNNCVGSEV
7128	2	5228	GRVDLWTLGLRSALRELSQIEAEIHKHWRRLLEGLSYYKPPSP SSAEKVKANKDVASPLKEGLRISKEFLGLDEEQSVQLQCYLQE DYGCTRDSVKTVLQDERQSQAL1LKIADYYEERTCILRCVLLH LTYFQDERHPYRVEYADCVKLEKEVLVKSYRQPEELYKTEAPT WETHGNLIMTERQVSFRWFVQCLREQSMMLIEIIFLYYAYFEMAPSD LLVLTKMFKEQGFGSRQTNRHVLDETMDPFVDRIGYFSALILVE GMDIESIHKCALDDRRELQFAODGLICQDMDCMLMTFGDIPHR APVILLA WALLRHTLNPEETSSVVRKIGGTIAIOLNVFOYLTRLQ SLASGGNDCTTSTACMVCYGLLSFVLTSLLEHTLGNQDDIIBTA CEVLADPSLPELFWGTEPTSGLGIIIDDSVCGMFPHLLSPLLQLL RALVSGKSTAKKVSYFLDKMSFYNELYKHKP HDVISHEDGTLWR RQTPKLLYPLGGQTNLRIIPQGTGVQVMLDDRAYLVRNEYSYSSW TLFTCEIEMLLHVVSTADVIQHQCQRVKPIIDLVHKVISTDLSIA DCLLPITSRIYMLLQRLITVISPVDVIASCVNCLTVLAARNPA KWTDLRHTGFLFVVAHPVSSLSQMSIAEGMNAAGGYGNILMNSE OPOGEYGVTLIAFLRLITTLVKGOLGSTQS0GLVPCVMFVLKEMI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PSYHKWRYNSHGVREQIGCLILELHAILNLCHETDLHSSHTPS LOFLC1CSLAVTEAGQTVINIMIGIVDTIDMVMAAQPRSDGAEG OGQGOLLIKTVKLAFLPSVTNNVIRLKPPSNVVSPLQEALSOHGAH GNNLIAVLAKYIYHKHDPALPRLA1QLLKRLATVAPMSVYACLG NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTV\AETQP GLIELFLNLEVKGDG\SDGSKEFSLGMW\SCLHAV\WVLEIDSQQ ODRYWCPPLLHRAAAIAFLHALWQDRRDSAMLVLRTPKFWENLT SPLFGT1SPPSETSEPSILETCALMKIICLEIYYYVKGSLDQP LKDTLKKFSIEKFAYVSKVSLAVHVAETEGSSCTSLLLEYQM LVAWRMLLIIATTHADIMHLDTSVVRQLFLDVLDGKALLLV PASVNCLRLGSMKCTLILLILLROWKRELGSVDEIILGPLTEILEG VLOAQDQQLMEKTKAKVFSAFITVLQMKEKVSDIPQYSQVLNV CETLQEVEIALFDQTRHSLALGSATEDKDSMETDDDCSRSRHRDQ RDGVCVGLGLHAKELCEVDDEGDSWLQVTRRLPILPTLTTLEV SLRMKONLHFTEATLHLLLTARTQQGATAVAGAGITQSICLPL LSVYQLSTNGTAQTPSASRKSDLAPSWPGVYRLSMSLMEQLLKT LRYNLFPEALDFVGVHQLCNAVRTVQSLACLEEAHTVG FILQLSNFMKEWHFHLPQLMRDIQVNGLYLCACTSFLHSRKML QHYLQNKNQGDGLPSAV\AQRV\QRPPSAASAPPSSKQPAADTE ASEQQALHTVQYGLLKILSKTLAALRHFPTDVCQIILLDQSLDLA EYNFLFALSFTTPTFDSEVAPSFGTLLLATVNVALNMLGEELDKK EPLTQAVGLSTOAEGTRTLKSLLMFTMENCYLLISQAMRYLRD PAVHPRDKQRMKQELSSSELSTLLSRYFRRGAPSSPATGVLP SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR
7129	1	1054	FRRFRWRRRLH*AGPAGASSAGCSPGEASGTMGSGELPPNINIKEPR WDQSTF1GRANHFFTVDPRNILLTNEQLESARKIVHDYRQGIV PPGLTENELWRAKYIYDSAFHPDTGEKMLIGRMSAQVPMNMTI TGCMMTFYRTTPAVLFQWQNTNQSFNAVVNVNTNRSGDAPLTVNEL GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPPFAAVAAACI NIPLMRQRELKVGIPVTDENGRLGESANAAKOAITQVVVSRL MAAPGMAIPPFIMNTLEKKFLKRFPMWSAPIOVGLVGFCLVFA TPLCCALFPQKSSMSVTSLEAELOQAKIQESHPELRRVYFNKG
7130	2	760	HEVPSLQTSDPLPGSVQRCSVVVSPQPKENWCCDHLYNSLGRKG ISAKSQPYHRSQSSSVLINKSMDSINYPDSVGKQQQLLSLHRSS RCESHQDLPIDIADSHQGTEKLSDLTLQDSQKVVVNRNLFLN AQIATQNSFSNFKETDGEDEDDYVEIKSEEDSELELSHNRRLKS DSKFVDAFDPSDNVCSGNTLHSLSNPRTPKKPVNSKLGSPYLTP YNDSDKLNDYLWRGPSPNQONIVOSLREKFQCLSSSSFA
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPPLDAVQFNHLEVV KLLQDYQDSYTLSETQAEAAAALSKENLESMV
7132	1420	1067	IDMLLLSCALVSGPYTLITTAWSADLGTTHKSLKGNAHALSTVTA IIDGTTGSVGAALGPLLAGLSPSGWSNVFYMLMFADACALLFLI RLIHKELSCPGSATGDQVPFKEQ
7133	2	3648	QQ1PGLLPAHGESGSDALRKPRLQKPKITGHLLDDLFPTLPSLEKF EEELLEHVQDHFQEGCGPLDGGALEI1ERRLRVGVHNGLGFVQ RPQVVVLVPEMDVALTRSASFSRKVVSSKTSQGSQALVRSRL RLPEMVGHPAFAVIFQLEXYFSSPAGVDGNAASVTSLSNLACMH MVRWAVWNPLLEADSGRVTPLQGGIQPNPSHCLVYKPSASMS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRK PTSPSSPPAVPVRVLAAPQNSPVGPGLSISQLAASPRSPTOHCL ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVUGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPKQKEESDCLOSNEMVQLFLAFS RVAQDCRGTSWPKTVYFTFQFYRFPATTPLQLVQLDEAGQPS SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGERRCFA RYLAVQTLQIDVWDGDSLLIGSAAVQMKHLLRQGRPAVQASHE

SEC ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEVVATEYEQDNMVSQGDMLGFGRVKPIGVHSVVKGRLLHTLAN VGHPCCEQKVVRGCASTLPPSRSLVINSNDGASRFSGSLLTTGSSRR KHVVQAAQKLADVDSELAAMLLTHARQGKPGQDVSRRESDATRRRK LERMRSRVLOQEAGGLGRRGCTSVLAQSVRTOHQLRLQVIAAYR ERTKAESIASLSSLATITTEHTLHATLGVAEFFEFVVLKNPHNTOH TVTVEIDNPPELSVIVDSDQEWRFKGAAGLHTPVEEDMFHRLRGSL APQLYLRLPHETAIVPPKQFSAGQLAQMVQASPGLSNEKGMDAV SPWKSSAVPTKGAKVLFRAASGGKPIAVLCLTVLQPHVVDQVFR FYHPELSFLKKAJRLPPWHTFPGAPVGMGLGEDPPVHVRCSDPNV ICETQNVPGEPRDIFLKVVASGSPSPEIKDFFVIIYSDRWLATPT OTWQVYHSLQORVDVSCVAGOLTRLSLVLRGQTQVRLVRAFTSH PQEELKTDPKGVFVLPPRGVQDILHVGVRPLRAGSREFVHLNLVDW CHQLVASLWVCLCCRQPLISKAFFEIMLAAGEGKGVNKRITYTNP YPSRRTFHLHSDHPELLRFREDSPFQVGGGETYTIGLQFAPSQRV GEELIYIYINDHEDKNEEAFCVKVIYQ
7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHVVLLEVHYDNPTYEGLIDNSG LRLFYTMDIRKYDAGVIEAGLWVSLFHTPPGMPEFOSEGHCTL ECLEEALAEAKPSGIHVFAVLLAHALAGRGIRLRLFRKGKEMKL LAYDDDFDFFNFOEFQYVKEEOTILPGDNLITECRYNTKDRADM WGGLSTRSEMCMLSLLYYPRINLTCASIPDIMEQLQFIGVKEI YRPVTTWPFIJKSPKQYKNNLSFMDAMNKFKWTKKEGLSFNKLVL SLPVNVRCSTKDNEWSI0GMLTALPPDIERPYKAEPPLVCGTSSS SSLHRDFSINLLVCLLSCLSTKSL
7135	2	2072	FVPRVTPRSLSLOGFKGESVGSITQPLPSSYLIFRAASESDGR WLDALELALRCSSLRLRGTCPKGRDGEPTSPDASPPSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDOSETPGAPVVRGTTVVEQVQEEELGEAEQSVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPPTFVLEPRSFINKLSDYYH ADLLSRAAVEEDAYSRMKVLVRWYLSGFYKKPKGIKPPYNPILG ETFRCCWFPHQTDRTFYIAE0VSHPPVSAFHVSNRKDGFCS GSITAKSRFYGNLSLALLDGKATLTFLNRAEDYTLTMYPAHKCG ILYGTMTLELGGKVTEIACAKNNFQAQLEFKLKPFFGGSTSINOI SGKITSGEEVILASLSGHWDRDVFKEEGSGSSALFWTPSGEVVR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRTQEKFAL EEAQRORARERQESLMPWPKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSAZTESSGSTPESCPELSDEEQDGFVPGGESPC PRCRKEARRLQALHEALISIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK
7136	2	418	DFVPSFRRPSGNTSQTWLLRATLKEVAGLREKIHLLDDMLK SQQRKVQRMIEQQLQNSKAVIOSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQ1SHGNFSTQARAKTENPGSIRISKPPSPKPMV IRVET
7137	2	466	WASGMSTVPGGSRHSLGIVQVRGGWGVGTGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLLRKQKGGVVPPFLGDFLTTELQRQLDSAI PDDLDGNTNKRKSKEVRVLOEMOLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIVQVRGGWGVGTGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLLRKQKGGVVPPFLGDFLTTELQRQLDSAI PDDLDGNTNKRKSKEVRVLOEMOLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7139	1	357	SLRNSARGLKMAAECARGAAALRRSINOPVAFVRRIPWTAASSQ LKEHFAQFGHVRCILPFDKETGFHRLGLGWVQFSSEEGLRNALQ QENHIIIDGVKVQVHTRPKLPQTSDEDEKKDF
7140	1401	1957	RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCPCSF NMNVSLKEQLRPSCPWPQGKCRKTPGNEEARPKAQDRLRGDLGKT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \=possible nucleotide insertion)
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKGQDPLMFSEDYQKSLLEQYHGLDQKLRKYVVGELIWNF ADFMTNQCG
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVLL VTPEKPLRRLGLSHRSRDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFLKDSP VRDLLPTVNSLTRSTPS/LKOPDASTPE***EGVSOQSPGYIWK EALQHEEGVTHLQSVPICIOKPSI FSS\SRSTPPVGRAGPSGRA AASEETRAAKLRLGAAKSSCOLPIPSAI PRPASRMLTSRSVPP GRGALPPDSLSTRKGLPRTAGHRVRESGHKVPSQRLNLPVM GATRSNLQPP
7142	658	839	LIFMLHMLKMLSSVTLHIRAFLYWICLKPTSCLI FQNVNLNLL KK*SRAVGVVVVVMCRT/YSSDLQVGVIKPWLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVILVHCNA
7143	3	773	SLEMSSDGEPLSRMDESDSISSTIMDVDTSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCWQCOACFNNSPDLDHRSIHVDGQRGG VFVCLWKCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASOGGLARHVPTHSQONNSKVSSQPKAKEEPSPKAGMNRR KLNKRNRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQ1KYKTLQKNISTIISKSLSKI
7144	1	988	FRVNMQDGGPSPAEHSKAEEESAGMEARFLGLPDAAAGSSGPTPAR RCPAPRPGAVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVNAHKGFCMSTLRTHKDYVKALAYAKDKEVVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLNRDGTQCLS GSSDGTIRLWSLGQORCIATYRVHDEGVWALQVNDAFTHVYSGG RDRKIYCTDLRNPDIRVLC

TRADOCs:1416260.1(%CSK01!.DOC)

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.

11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
  - a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
  - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
  - a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00  
 US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
 U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
 MEDLINE, EAST

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992). see especially columns 3-18.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256. see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256. HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883. BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289. HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.	1-11, 13-16, and 19-26

<input type="checkbox"/>	Further documents are listed in the continuation of Box C.	<input type="checkbox"/>	See patent family annex.
* A	Special categories of cited documents:	* T *	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
* A	document defining the general state of the art which is not considered to be of particular relevance	* X *	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
* E	earlier application or patent published on or after the international filing date	* Y *	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
* L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	* & *	document member of the same patent family
* O	document referring to an oral disclosure, use, exhibition or other means		
* P	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search	Date of mailing of the international search report <i>07 JUN 2001</i>
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized office: <i>Michael Woodward</i> Michael Woodward Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

international application No.

PCT/US00/34263

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
This includes 4 invention Groups and 3572 sequence species

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

  

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of identifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containing same, respectively, and methods of making as well as the first method of use of this subject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group II as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different method than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

## CORRECTED VERSION

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
26 July 2001 (26.07.2001)

PCT

(10) International Publication Number  
WO 01/53312 A1(51) International Patent Classification<sup>7</sup>: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00

(21) International Application Number: PCT/US00/34263

(22) International Filing Date:  
26 December 2000 (26.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  

09/471,275	23 December 1999 (23.12.1999)	US
09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/552,317 (CIP)
Filed on	25 April 2000 (25.04.2000)
US	09/598,042 (CIP)
Filed on	9 July 2000 (09.07.2000)
US	09/620,312 (CIP)
Filed on	19 July 2000 (19.07.2000)
US	09/653,450 (CIP)
Filed on	3 August 2000 (03.08.2000)
US	09/662,191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693,036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).

LIU, Chenghua [CN/US]; 1125 Rancho Way #14, San Jose, CA 95117 (US). ASUNDI, Vinod [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). CHEN, Rui-hong [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). MA, Yunqing [CN/US]; 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). QIAN, Xiaohong, B. [CN/US]; 3662 Tumble Way, San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). WANG, Dunrui [CN/US]; 932 La Palma, Milpitas, CA 95035 (US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). WEHRMAN, Tom [US/US]; 3210 CCSR Mol Pharm, 269 W. Campus Drive, Stanford, CA 94305 (US). XU, Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). XUE, Aidong, J. [CN/US]; 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Campbell, CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping [CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US). GOODRICH, Ryle [US/US]; 4896 Sandy Lane, San Jose, CA 95124 (US). DRMANAC, Radoje, T. [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).

(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:  
— with international search report

[Continued on next page]

WO 01/53312 A1

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



(48) Date of publication of this corrected version:

1 November 2001

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(15) Information about Correction:

see PCT Gazette No. 44/2001 of 1 November 2001, Section  
II

## REVISED VERSION

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
26 July 2001 (26.07.2001)

PCT

(10) International Publication Number  
WO 01/53312 A1(51) International Patent Classification: C07H 21/04.  
C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00

(21) International Application Number: PCT/US00/34263

(22) International Filing Date:  
26 December 2000 (26.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  

09/471,275	23 December 1999 (23.12.1999)	US
09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/552,317 (CIP)
Filed on	25 April 2000 (25.04.2000)
US	09/598,042 (CIP)
Filed on	9 July 2000 (09.07.2000)
US	09/620,312 (CIP)
Filed on	19 July 2000 (19.07.2000)
US	09/653,450 (CIP)
Filed on	3 August 2000 (03.08.2000)
US	09/662,191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693,036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).

LIU, Chenghua [CN/US]; 1125 Ranchero Way #14, San Jose, CA 95117 (US). ASUNDI, Vinod [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). CHEN, Rui-hong [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). MA, Yunqing [CN/US]; 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). QIAN, Xiaohong, B. [CN/US]; 3662 Tumble Way, San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). WANG, Dunrui [CN/US]; 932 La Palma, Milpitas, CA 95035 (US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). WEHRMAN, Tom [US/US]; 3210 CCSR Mol Pharm, 269 W. Campus Drive, Stanford, CA 94305 (US). XU, Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). XUE, Aidong, J. [CN/US]; 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Campbell, CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping [CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US). GOODRICH, Ryle [US/US]; 4896 Sandy Lane, San Jose, CA 95124 (US). DRMANAC, Radoje, T. [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).

(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:  
— with international search report

[Continued on next page]

WO 01/53312 A1

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



(88) Date of publication of the revised international search report: 20 June 2002

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(15) Information about Corrections:

see PCT Gazette No. 25/2002 of 20 June 2002, Section II

Previous Correction:

see PCT Gazette No. 44/2001 of 1 November 2001, Section II

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
MEDLINE, EAST

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon ( <i>Papio anubis</i> ). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.	1-11, 13-16, and 19-26

 Further documents are listed in the continuation of Box C

See patent family annex.

Special categories of cited documents:		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority (claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

Date of mailing of the international search report

05 SEP 2001

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231  
Facsimile No. (703)305-3230Authorized officer  
Michael Woodward

Telephone No. (703)308-0196

**Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:  
This includes 4 invention Groups and 3572 sequence species

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11, 13-16, and 19-26

Remark on Protest

  

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of identifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containing same, respectively, and methods of making as well as the first method of use of this subject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different method than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

